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- GRAY SCALE DOCUMENTS

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SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,684
FILING DATE: No. 580640member 10, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,477
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 568630member 12, 1993
APPLICATION NUMBER: 09/040,952
APPLICATION NUMBER: 06/038,766
FILING DATE: March 24, 1993
APPLICATION NUMBER: 07/842,438
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Werburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION:
NAME: Werburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SOURCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
US-08-151-477A-4
Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 TTAGGG 6
DB 6 TTAGGG 1

RESULT 6
US-08-670-999-3
Patent No. 580644
Patent No. 584977
GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
TITLE OF INVENTION: Compositions and Methods for Altering
the Biodistribution of Biological Agents
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Los Angeles
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMMERCE/TRADE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
APPLICATION NUMBER: US/08/670,999
CURRENT APPLICATION DATA:
FILING DATE: March 24, 1993
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
TELEPHONE: 515-288-3667
TELECOMMUNICATION INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
TELEPHONE: 515-288-3667
INFORMATION FOR SEQ ID NO: 3:
SOURCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOHETICAL: NO

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,684
FILING DATE: No. 580640member 10, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,477
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 568630member 12, 1993
APPLICATION NUMBER: 09/040,952
APPLICATION NUMBER: 06/038,766
FILING DATE: March 24, 1993
APPLICATION NUMBER: 07/842,438
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Werburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION:
NAME: Werburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SOURCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
US-08-151-477A-4/C
Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 TTAGGG 6
DB 6 TTAGGG 6

RESULT 5
US-08-151-477A-4/C
Sequence 4, Application US/08151477A
Patent No. 580644
Patent No. 584977
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Michael D. Jackson
APPLICANT: Nam Moo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weirach
APPLICANT: Michael J. McChern
APPLICANT: Hameyoun Vaziri
APPLICANT: Therapies and Diagnostics of
the Human Genome
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
THE HUMAN GENOME
CORRESPONDENCE ADDRESS:
ADDRESSEE:
STREET: 633 West Fifth Street
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94011
COMMERCE/TRADE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

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ANTI-SENSE: YES
US-08-670-593-3
Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 7
US-08-729-598-4
: Sequence 4, Application US/08729598
: Patent No. 60016570N
: APPLICANT: Hardin, Charles C.
: APPLICANT: Brown II, Bernard A.
: APPLICANT: Roberts, John J.
: APPLICANT: Roberts, John A.
: TITLE OF INVENTION: Antibodies that Selectively Bind
: TITLE OF INVENTION: Quadruplex Nucleic Acid
: CORRESPONDENT ADDRESS: 13
: ADDRESS: Sorcjin J. Biwas
: STREET: P.O. Box 37428
: CITY: Raleigh, NC 27627
: STATE: NC 60016570th Carolina
: COUNTRY: USA
: ZIP: 27627
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA: US/08/729-598
: APPLICATION NUMBER: US/08/729-598
: CLASSIFICATION: 5.0
: ATTORNEY/AGENT INFORMATION:
: NAME: Biwas, Sorcjin J.
: REFERENCE/DOCKET NUMBER: 5051-301A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 854-1400
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 base pairs
: STRANDS: 2
: TOPOLOGY: single
: QUERY MATCH 100.0%; Score 6; DB 3; Length 6;
: BEST LOCAL SIMILARITY 100.0%; Pred. No. 6.8e+07;
: MATCHES 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 1 TTAGGG 6

US-08-819-867-9
: Sequence 27, Application US/08819867
: Patent No. 6007989
: GENERAL INFORMATION:
: APPLICANT: Calvin D. West
: APPLICANT: Scott L. Weinrich
: APPLICANT: Michael W. Strahl
: APPLICANT: Jerry Shay
: APPLICANT: Woodring E. Wright
: APPLICANT: Elizabeth H. Blackburn

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APPLICANT: Catherine W. Strahl
APPLICANT: Michael W. Strahl
APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Homayoun Vaziri
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
: TITLE OF INVENTION: CONJUGATED ANTIBODIES
: TITLE OF INVENTION: TELOMERE LENGTH AND/OR
: TITLE OF INVENTION: TELOMERASE ACTIVITY
: NUMBER OF SEQUENCES: 80
: CORRESPONDENT ADDRESS: 80
: ADDRESS: Lyon & Lyon
: STREET: 633 West Fifth Street
: CITY: Suite 4700
: STATE: California
: COUNTRY: U.S.A.
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: CONVERTED HEADINGS FROM:
: MEDIUM TYPE: e-ecode
: OPERATING SYSTEM: IBM PC, DOS 5.0
: SOFTWARE: Fastseq for Windows 2.0
: CURRENT APPLICATION DATA: US/08/819-867
: APPLICATION NUMBER: US/08/819-867
: FILING DATE: March 14, 1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/153,051
: FILING DATE: No. 6007989ember 12, 1993
: APPLICATION NUMBER:
: FILING DATE: INFORMATION:
: NAME: Chambers, Daniel M.
: REFERENCE/DOCKET NUMBER: 224/232
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 base pairs
: STRANDS: 2
: TOPOLOGY: linear
: US-08-819-867-9
: QUERY MATCH 100.0%; Score 6; DB 3; Length 6;
: BEST LOCAL SIMILARITY 100.0%; Pred. No. 6.8e+07;
: MATCHES 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 9
US-08-819-867-9
: Sequence 27, Application US/08819867
: Patent No. 6007989
: GENERAL INFORMATION:
: APPLICANT: Calvin D. West
: APPLICANT: Scott L. Weinrich
: APPLICANT: Michael W. Strahl
: APPLICANT: Jerry Shay
: APPLICANT: Woodring E. Wright
: APPLICANT: Elizabeth H. Blackburn

```

APPLICANT: Nam Youn Kim
 APPLICANT: Homyoun Vaziri
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 CONDITIONS RELATED TO
 TITLE OF INVENTION: TETRAHYDRO-2H-PYRAN-2-OL
 TITLE OF INVENTION: TELOMERASE ACTIVITY
 NUMBER OF SEQUENCES: 80
 CURRENT APPLICATION DATA:
 ADDRESS: Lyons, Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.

COMPUTER: 98050606 FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 OPERATING SYSTEM: IBM PC DOS 5.0
 SOFTWARE: FASTSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 FILING DATE: 08/09/1997
 FILING DATE: March 14, 1997

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 FILING DATE: 08/15/051
 FILING DATE: No. 600798568
 APPLICATION NUMBER: 224/232
 NAME: Chambers, Daniel M.
 REGISTRATION NUMBER: 34,561
 REFERENCE/DOCKET NUMBER: 224/232
 TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 27:
 LENGTH: 6 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear

Query Match 100.0%; Score 6; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6; 0e+07;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTACGG 6
 6 TTACGG 1

RESULT 10 0198-1
 Sequence 1: Application US/08630019A
 GENERAL INFORMATION: JERRY M.
 APPLICANT: Wright, Woodring E.
 APPLICANT: Pietysek, Mieczyslaw A.
 APPLICANT: Corey, David
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by
 Peptide Nucleic Acids
 NUMBER OF SEQUENCES: 46
 CURRENT APPLICATION DATA:
 ADDRESS: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California

COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 09-JUN-1996

CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 FILING DATE: 08/09/630,019A
 APPLICATION NUMBER: 015389-001600US
 NAME: Scovella, John
 REGISTRATION NUMBER: 32,944
 REFERENCE/DOCKET NUMBER: 015389-001600US

TELEPHONE: (415) 576-0300
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 1:
 LENGTH: 6 base pairs
 TYPE: nucleic acid
 TOPOLOGY: single

MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "peptide nucleic acid (PNA).
 DESCRIPTION: /desc = "peptide nucleic acid (PNA).
 DESCRIPTION: Nucleic acid phosphate linkages are released by
 treatment with phosphatase. The resulting PNA can be linked to a
 target nucleic acid through a methylene carbonyl linker"

US-08-030-019A-1
 Query Match 100.0%; Score 6; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6; 8e+07;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGG 6

DB 1 TTACGG 6

RESULT 11
 US-08-018-545-3
 Sequence 1: Application US/09018545
 GENERAL INFORMATION: Richard T.
 APPLICANT: Hurley, Laurence R.
 TITLE OF INVENTION: INHIBITORS
 TITLE OF INVENTION: INHIBITORS
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/018-545
 FILING DATE: Concurrently Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/037,295
 FILING DATE: 07/07/97
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: US98,654

TELECOMMUNICATION INFORMATION:

TELEPHONE (512) 418-3000
TELEFAX (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE LENGTH: 1000
LENGTH: 1000
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-018-545-3

Query Match 100.0% Score 6; DB 3; Length 6;
Best Local Similarity 100.0% Prod No. 6-8e+07; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

1 TTAGGG 6
1 TTTAGGG 6

RESULT 12
US-09-114-399-3

Sequence 3: Application US/0914399

GENERAL INFORMATION:

APPLICANT: Porter, Thomas R.

APPLICANT: Iversen, Perick L.

TITLE OF INVENTION: Targeted Site Specific Drug Delivery

TITLE OF INVENTION: Compositions and Method of Use

SEQUENCE ID NO: 3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399-3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399-3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399-3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399-3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399-3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399-3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-114-399-3

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

FILE REFERENCE: 055/003

CURRENT APPLICATION NUMBER: US/09/608,636A

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US/00/442,173

PRIOR APPLICATION NUMBER: JP 11-187616

PRIOR FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: JP 11-307576

PRIOR APPLICATION NUMBER: US/99/018,999-10-26

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent in version 3.1

SEQUENCE ID NO: 1

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: DNA

ORGANISM: Artificial Sequence

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: oligonucleotide

OTHER INFORMATION: oligonucleotide

US-09-608-636A-1

Query Match 100.0% Score 6; DB 4; Length 6;

Best Local Similarity 100.0% Prod No. 6-8e+07; Indels 0;

Matches 6; Conservative 0; Mismatches 0;

1 TTAGGG 6

1 TTTAGGG 6

RESULT 14

US-09-378-535-9

Sequence 9: Application US/09378535

SEQUENCE ID NO: 9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

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SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

SEQUENCE TOPOLOGY: linear

SEQUENCE US-09-378-535-9

SEQUENCE LENGTH: 1000

SEQUENCE TYPE: nucleic acid

SEQUENCE STRANDEDNESS: single

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

CONDITIONS RELATED TO

TELOMERASE ACTIVITY

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TELOMERASE ACTIVITY

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-378-535-27
Query Match
Best Local Similarity: 100.0%; Score 6; DB 4; length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
1 TTAGGG 6

SEQUENT 15
US-09-378-535-27/c
Sequence 27, Application US/09178535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Michael J. Meschery
Michael J. Meschery

Jerry Shay
Wendell E. Wright
Rudolph C. Bachmann
Nam Woo Kim
Honeyoun Vaziri

TITLE OF INVENTION: METHODS AND DIAGNOSTIC OF
TECHNIQUES FOR THE IDENTIFICATION OF
CONDITIONS RELATED TO
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90070
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/09/378.535
APPLICATION NUMBER: US/09/378.535
FILING DATE: 20-AUG-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION NUMBER: 08/819,867

ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-378-535-27

Query Match
Best Local Similarity: 100.0%; Score 6; DB 4; length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
DB 6 TTAGGG 1

Search completed: January 1, 2004, 00:32:19
Job time : 23.4276 secs

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00, Search time 69.9464 Seconds

Title: US-09-540-843-11
Sequence: 1 ttgggg 6
Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 263441 seqs, 170637950 residues
Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 30
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Lifting files: 45 summaries

Database: Published Applications, Na.:
1: /csm2_6/prodata/1/pubna/US07_PUBCOMB.seq.
2: /csm2_6/prodata/1/pubna/US08_PUBCOMB.seq.
3: /csm2_6/prodata/1/pubna/US09_PUBCOMB.seq.
4: /csm2_6/prodata/1/pubna/US06_PUBCOMB.seq.
5: /csm2_6/prodata/1/pubna/US05_PUBCOMB.seq.
6: /csm2_6/prodata/1/pubna/US04_PUBCOMB.seq.
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9: /csm2_6/prodata/1/pubna/US01_PUBCOMB.seq.
10: /csm2_6/prodata/1/pubna/US00_PUBCOMB.seq.
11: /csm2_6/prodata/1/pubna/US99_PUBCOMB.seq.
12: /csm2_6/prodata/1/pubna/US98_PUBCOMB.seq.
13: /csm2_6/prodata/1/pubna/US97_PUBCOMB.seq.
14: /csm2_6/prodata/1/pubna/US96_PUBCOMB.seq.
15: /csm2_6/prodata/1/pubna/US95_PUBCOMB.seq.
16: /csm2_6/prodata/1/pubna/US94_PUBCOMB.seq.
17: /csm2_6/prodata/1/pubna/US93_PUBCOMB.seq.
18: /csm2_6/prodata/1/pubna/US92_PUBCOMB.seq.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
1	6	100.0	6	9	US-09-817-387-29	Sequence 29, Appl
2	6	100.0	6	9	US-09-735-363A-49	Sequence 49, Appl
3	6	100.0	6	10	US-09-730-993-4	Sequence 4, Appl
4	6	100.0	6	11	US-09-940-171A-6	Sequence 6, Appl
5	6	100.0	6	13	US-10-255-535-8	Sequence 8, Appl
6	6	100.0	6	13	US-10-336-265-1	Sequence 1, Appl
7	6	100.0	6	13	US-10-336-265-1	Sequence 1, Appl
8	6	100.0	6	13	US-10-336-265-4	Sequence 4, Appl
9	6	100.0	6	13	US-10-336-265-6	Sequence 6, Appl
10	6	100.0	6	13	US-10-336-265-6	Sequence 6, Appl
11	6	100.0	6	13	US-10-336-265-6	Sequence 6, Appl
12	6	100.0	6	13	US-10-232-927A-27	Sequence 27, Appl
13	6	100.0	6	15	US-10-122-630-11	Sequence 11, Appl
14	6	100.0	6	15	US-10-122-630-12	Sequence 12, Appl
15	6	100.0	6	15	US-10-122-630-11	Sequence 11, Appl

C 17 6 100.0 6 15 US-10-122-633-12 Sequence 12, Appl

18 6 100.0 7 10 US-09-730-993-4 Sequence 4, Appl

19 6 100.0 7 11 US-09-940-171A-6 Sequence 6, Appl

20 6 100.0 8 13 US-10-255-535-8 Sequence 8, Appl

21 6 100.0 8 13 US-10-336-265-58 Sequence 58, Appl

22 6 100.0 9 10 US-09-728-57A-19 Sequence 19, Appl

23 6 100.0 10 13 US-10-330-627-1286 Sequence 1287, Ap

24 6 100.0 10 13 US-10-330-627-1287 Sequence 1287, Ap

25 6 100.0 10 13 US-10-330-627-1289 Sequence 1289, Ap

26 6 100.0 10 13 US-10-330-627-1439 Sequence 1439, Ap

27 6 100.0 10 13 US-10-330-627-1439 Sequence 1439, Ap

28 6 100.0 10 14 US-10-033-145-56 Sequence 56, Appl

29 6 100.0 10 14 US-10-033-145-56 Sequence 56, Appl

30 6 100.0 10 14 US-10-033-145-58 Sequence 58, Appl

31 6 100.0 10 14 US-10-033-145-58 Sequence 58, Appl

32 6 100.0 10 14 US-10-033-145-58 Sequence 58, Appl

33 6 100.0 10 15 US-10-044-692A-294 Sequence 294, Appl

34 6 100.0 10 15 US-10-044-692A-294 Sequence 294, Appl

35 6 100.0 11 11 US-09-835-370-63 Sequence 63, Appl

36 6 100.0 11 11 US-09-249-155-57 Sequence 57, Appl

37 6 100.0 11 11 US-09-249-155-57 Sequence 57, Appl

38 6 100.0 11 11 US-09-942-310-74 Sequence 74, Appl

39 6 100.0 11 12 US-10-334-322-57 Sequence 57, Appl

40 6 100.0 11 12 US-10-334-322-57 Sequence 57, Appl

41 6 100.0 11 12 US-10-334-322-271 Sequence 271, Appl

42 6 100.0 11 13 US-10-255-535-14 Sequence 14, Appl

43 6 100.0 11 13 US-10-255-535-14 Sequence 14, Appl

44 6 100.0 11 13 US-10-359-935-2 Sequence 2, Appl

45 6 100.0 11 15 US-10-122-630-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
Sequence 29, Application US/09817387
GENERAL INFORMATION:
APPLICANT: Max-Debruck-Centric fur Molekulare Medizin
FILE REFERENCE: US/09817387
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQUENCE 1:
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: telomeric
OTHER INFORMATION: DNA of man
US-09-817-387-29

Query Match 100.0% Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatch 0; Indels 0; Gaps 0;
Oy 1 TTAGGG 6
Db 1 TTAGGG 6
RESULT 2
US-09-817-387-29
Sequence 49, Application US/09735363A
Patent No. US20010041683A1
GENERAL INFORMATION:
APPLICANT: Fillon, Mario

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APPLICANT: SALAZAR, MIGUEL
APPLICANT: HIRLEY, LAURENCE H.
INVENTOR: HIRLEY, LAURENCE H.
TITLE OF INVENTION: CATALYTIC-INDUCED HYPERMETHYLATION OF DNA
FILE NUMBER: US 09/540-173A
CURRENT APPLICATION NUMBER: US/09/540-173A
PRIOR APPLICATION NUMBER: 08/0730,893
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 08/244,675
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 06/073,629
PRIOR FILING DATE: 1996-04-02
NUMBER OF SEQ ID NOS: 12
SEQUENCE LISTING: Patent in Ver. 2.1
LENGTH: 6
TYPE: DNA
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-540-173A-1
Query Match 100.0%, Score 6; DB 11; Length 6;
Best Local Similarity 100.0%, Fwd. No. 5;e+00;
Matches 6; Conservative 0; Mismatch 0; Indels 0;
AY 1 TTAGGG 6
BD 1 TTAGGG 6
RESULT 5
Sequence 8, Application US/1025535
Publication No. US20030180141
GENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: Gvozdenov, Sergei
APPLICANT: Pogorzala, Krzyszina
APPLICANT: Nolan, Gerald L.
APPLICANT: Molnar, Gordon
TITLE OF INVENTION: Oligonucleotide Conjugates
FILE REFERENCE: 072/0029
CURRENT APPLICATION NUMBER: US/10/255,535
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: PCT/US02/09118
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 00/276,322
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: patent in version 3.1
SEQUENCE NO 8
TYPE: DNA

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FEATURE:
  OTHER INFORMATION: oligonucleotide
  US-10-255-535-8
  Query Match      100.0%; Score 6; DB 13; Length 6;
  Best Local Similarity 100.0%; Pred. NO. 5.6e+08;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Oy      1 TTAGGG 6
          |||||
          1 TTAGGG 6
  Db
  ASSEUR 6
  US-10-255-3
  Sequence Application US/4034265

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Copied from 09980559 on 05/19/2004

Publication No. US2003014898A1

GENERAL INFORMATION:
 APPLICANT: Kool, Eric T.
 TITLE OF INVENTION: Telomere Encoding Synthetic DNA Nanocircles, and their use for
 the Elongation of Telomere Repeats
 FILE REFERENCE: 12665.0021.NPHS01
 CURRENT APPLICATION NUMBER: US/10/336,265
 PRIORITY FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: US 60/345,056
 PRIOR FILING DATE: 2002-01-04
 NUMBER OF SEQ ID NOS: 64
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: Patent in version 3.2

LENGTH: 6

TYPE: RNA

ORGANISM: Homo sapiens

US-10-336-265-1

Query Match 100.0%; Score 6; DB 13; Length 6;

Best Local Similarity 100.0%; Pred. No. 5.6e+08; DB 13; Length 6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6

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Publication No. US2003014898A1

GENERAL INFORMATION:
 APPLICANT: Kool, Eric T.
 TITLE OF INVENTION: Telomere Encoding Synthetic DNA Nanocircles, and their use for
 the Elongation of Telomere Repeats
 FILE REFERENCE: 12665.0021.NPHS01
 CURRENT APPLICATION NUMBER: US/10/336,265
 PRIORITY FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: US 60/345,056
 PRIOR FILING DATE: 2002-01-04
 NUMBER OF SEQ ID NOS: 64
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: Patent in version 3.2

LENGTH: 6

TYPE: RNA

ORGANISM: Homo sapiens

US-10-336-265-4

Query Match 100.0%; Score 6; DB 13; Length 6;

Best Local Similarity 100.0%; Pred. No. 5.6e+08; DB 13; Length 6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6

1 TTAGGG 6

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Publication No. US2003014898A1

GENERAL INFORMATION:
 APPLICANT: Kool, Eric T.
 TITLE OF INVENTION: Telomere Encoding Synthetic DNA Nanocircles, and their use for
 the Elongation of Telomere Repeats
 FILE REFERENCE: 12665.0021.NPHS01
 CURRENT APPLICATION NUMBER: US/10/336,265
 PRIORITY FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: US 60/345,056
 PRIOR FILING DATE: 2002-01-04
 NUMBER OF SEQ ID NOS: 64
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: Patent in version 3.2

LENGTH: 6

TYPE: RNA

ORGANISM: Homo sapiens

US-10-336-265-4

Query Match 100.0%; Score 6; DB 13; Length 6;

Best Local Similarity 100.0%; Pred. No. 5.6e+08; DB 13; Length 6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Publication No. US2003014898A1

GENERAL INFORMATION:
 APPLICANT: Kool, Eric T.
 TITLE OF INVENTION: Telomere Encoding Synthetic DNA Nanocircles, and their use for
 the Elongation of Telomere Repeats
 FILE REFERENCE: 12665.0021.NPHS01
 CURRENT APPLICATION NUMBER: US/10/336,265
 PRIORITY FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: US 60/345,056
 PRIOR FILING DATE: 2002-01-04
 NUMBER OF SEQ ID NOS: 64
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: Patent in version 3.2

LENGTH: 6

TYPE: RNA

ORGANISM: Homo sapiens

US-10-336-265-4

Query Match 100.0%; Score 6; DB 13; Length 6;

Best Local Similarity 100.0%; Pred. No. 5.6e+08; DB 13; Length 6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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APPLICANT: Yaar, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
PUBLICATION NO: US09030326/0A
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/467,012
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/0162
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQUENCE 1
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-11
Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-122-630-12/c
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
PUBLICATION NO: US09030326/0A
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/467,012
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/0162
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQUENCE 1
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-12
Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TTAGGG 6
1 TTAGGG 6

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DB 6 TTAGGG 1
RESULT 15
US-10-122-633-11
Sequence 11, Application US/10122633
PUBLICATION NO: US09030326/1A1
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/0162
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQUENCE 11
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-11
Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 TTAGGG 6
Job time : 89.9494 secs
Search completed: January 1, 2004, 01:10:39

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LOCUS       AM248926               21 bp     mRNA      linear      EST 07-JUN-2000
DEFINITION  NTH_MOC_7 Homo sapiens cDNA clone IMAGE:2821108 3'.
ACCESSION   AM248926
VERSION     1
KEYWORDS    NTH_MOC_7
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Carnivora; Cetartiodactyla; Hominoidea; Homo.

REFERENCE   1 (bases 1 to 21)
AUTHORS     Nih-MOC http://mhc.nci.nih.gov/
TITLES      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Other ESTs: 2821056 Sprime
            Contact: Robert Strausberg, Ph.D.
            Email: rstraus@nhi.nih.gov
            Project Name: Mammalian Gene Collection
            Project Description: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LMML at:
            http://www.ncbi.nlm.nih.gov/bioproject/1000000
            Trimming: cross match from University of Washington Genome Center
            PHRAP suite. Poly-T identification: betMatch.pl from Berkeley
            Drosophila Genome Project, University of Washington Genome Center;
            PHRAP suite. Poly-T identification: betMatch.pl from Berkeley
            Drosophila Genome Project, University of Washington Genome Center.
            Very Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: L1C65 row: N column: 1
            High quality sequence stop: 10
            Features:
            1..21
            Location/Qualifiers
            ..
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2821056"
            /cell_line="MGC-7"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NTH_MOC_7"
            /notes="Organ: lung; Vector: pOT79; Site: 1. XhoI; Site: 2.
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GCGACGAC(G). Site-selected 500bp for average
            tiling size 1. MGC library constructed by the Hong in
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
            BASE COUNT      4 a 3 c 3 g 11 t
            Query Match      100.0%; Score 6; DB 9; Length 21;
            Best Local Similarity 100.0%; Pred. No. 6.7e+05;
            Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTATGGG 6
Db      20 TTATGGG 15

Search completed, December 31, 2003, 19:41:30
Job time : 692.392 sec#

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EST. sapiens (human)
ORGANISM    Homo sapiens
            Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Carnivora; Cetartiodactyla; Hominoidea; Homo.

REFERENCE   1 (bases 1 to 21)
AUTHORS     Nih-MOC http://mhc.nci.nih.gov/
TITLES      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Other ESTs: 2821108 Sprime
            Contact: Robert Strausberg, Ph.D.
            Email: rstraus@nhi.nih.gov
            Project Name: Mammalian Gene Collection
            Project Description: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LMML at:
            http://www.ncbi.nlm.nih.gov/bioproject/1000000
            Trimming: cross match from University of Washington Genome Center
            PHRAP suite. Poly-T identification: betMatch.pl from Berkeley
            Drosophila Genome Project, University of Washington Genome Center;
            PHRAP suite. Poly-T identification: betMatch.pl from Berkeley
            Drosophila Genome Project, University of Washington Genome Center.
            Very Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: L1C65 row: P column: 5
            High quality sequence stop: 10
            Features:
            1..21
            Location/Qualifiers
            ..
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2821108"
            /cell_line="MGC-7"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NTH_MOC_7"
            /notes="Organ: lung; Vector: pOT79; Site: 1. XhoI; Site: 2.
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GCGACGAC(G). Site-selected 500bp for average
            tiling size 1. MGC library constructed by the Hong in
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
            BASE COUNT      4 a 6 c 0 g 11 t
            Query Match      100.0%; Score 6; DB 9; Length 21;
            Best Local Similarity 100.0%; Pred. No. 6.7e+05;
            Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTATGGG 6
Db      20 TTATGGG 15

Search completed, December 31, 2003, 19:41:30
Job time : 692.392 sec#

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/db_xref="taxon:10090"
/sex="Male"
/clone="U0C1M08BQJ04"
/ab_hosts="B. coli strain X110-Gold, T1-resistant, F-
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
electrophoresis. Vector DNA was prepared from a derivative
inducible derivative of plasmid R1. The vector was ligated
with appropriate BamHI and HindIII fragments. The vector was
purified. The sheared, adapted mouse DNA was annealed to
chemically competent E. coli X110-Gold (Stratagene) cells
and transformed into cells selected for ampicillin resistance.
BASE COUNT
ORIGIN      3 a 13 c 6 g 9 t
Query Match      100.0%; Score 6; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ct 1 TTAGGG 6
Gb 16 TTAGGG 11

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RESULT 8
DEFINITION 1M046710L Mouse 10kb plasmid U0C1M library Mus musculus genomic
clone U0C1M046710L R. genomic survey sequence.
ACCESSION A262717.1 GI:11749364
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dum, D., Ayoub, A., Barber, M., Bearson, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
Wang, D., Weiss, R.,
plasmid inserts
Mammalian genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT University of Utah Genome Center
Ref. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Tel.: 801 585 5606
Fax: 801 585 7177
Email: dum@genetics.utah.edu
Plate: 0467 Row: 0 Column: 10
Seq primer: CACACAGCAACATGATGACC
Class: plasmid ends
High quality sequence atcop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0C1M046710L"
/sex="Male"
/ab_hosts="B. coli strain X110-Gold, T1-resistant, F-
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
electrophoresis. Vector DNA was prepared from a derivative
inducible derivative of plasmid R1. The vector was ligated
with appropriate BamHI and HindIII fragments. The vector was
purified. The sheared, adapted mouse DNA was annealed to
chemically competent E. coli X110-Gold (Stratagene) cells
and transformed into cells selected for ampicillin resistance.
BASE COUNT
ORIGIN      5 a 2 c 7 g 6 t
Query Match      100.0%; Score 6; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ct 1 TTAGGG 6
Gb 13 TTAGGG 18

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RESULT 9
DEFINITION 1M0542017F Mouse 10kb plasmid U0C1M library Mus musculus genomic
clone U0C1M0542017 F. genomic survey sequence.
ACCESSION A262909
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dum, D., Ayoub, A., Barber, M., Bearson, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
Wang, D., Weiss, R.,
plasmid inserts
Mammalian genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT University of Utah Genome Center
Ref. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Tel.: 801 585 5606
Fax: 801 585 7177
Email: dum@genetics.utah.edu
Plate: 0467 Row: 0 Column: 10
Seq primer: CATTGTAACAGCCGACAT
Class: plasmid ends
High quality sequence atcop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"

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Copied from 09980559 on 05/19/2006


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XX Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 2 other;
SU Query Match 100.0%; Score 6; DB 23; Length 8;
Query Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGG 6
2 TTACGG 7

Db

RESULT 14
AAT05735
ID AAT05735 standard; DNA; 9 BP.
XX
XX AAT05735;
XX 01-FEB-1996 (first entry)
XX Telomerase oligonucleotide substrate #2.
XX Telomerase: proliferation; telomere; hybrid; immortalised cell; anaemia;
XX transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; as.
XX Synthetic.
XX W0951393-A1.
XX 18-MAY-1995.
XX 10-NOV-1994; 94W0-US1310.
XX 12-NOV-1993; 93US-0153051.
XX 12-NOV-1993; 93US-0151477.
XX (TEXA) UNIV TEXAS SYSTEM.
XX (GERO-) GERON CORP.
XX Shay J, West MD, Wright WE;
XX WPI; 1995-224051/29.
XX Increasing telomere length in cells - to increase proliferative
XX capacity and therefore delay cellular senescence, useful in cell
XX therapy and transplantation
XX Claim 12; Page 29; 38pp; English.
XX Oligonucleotide AAT05734.7 are examples of telomerase substrates used
XX to increase the proliferative capacity of normal cells that express
XX telomerase activity. The oligonucleotides allow an increase in
XX length of telomeres in normal cells and in hybrids of normal and
XX cancer cells. The oligonucleotides are used to increase the
XX capacity of cells to replicate esp. those treated ex vivo and used
XX for transplantation techniques e.g. cell therapy, for the treatment
XX of AIDS, anaemia, leukaemia or lymphoma.
XX Sequence 9 BP; 2 A; 0 C; 3 G; 4 T; 0 other;
SU Query Match 100.0%; Score 6; DB 16; Length 9;
Query Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGG 6
2 TTACGG 6

Db

RESULT 15
AAT89240
ID AAT89240 standard; DNA; 9 BP.
XX
XX AAT89240;
XX 12-MAY-1998 (first entry)
XX Peptide nucleic acid 15, targeted to mammalian telomerase.
XX Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridization;
XX inhibitor; as.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base /tag= a
XX /note= "Sugar-phosphate backbone has been replaced by
XX a peptide backbone"
XX W09718013-A1.
XX 16-OCT-1997.
XX 09-APR-1997; 97W0-US059311.
XX 09-APR-1996; 96US-0630019.
XX (GERO-) GERON CORP.
XX Corey D, Norton JC, Placyszak WA, Shay JW, Wright WE;
XX WPI; 1997-512647/47.
XX New peptide nucleic acids hybridising to mammalian telomerase RNA -
XX used to inhibit telomerase, for treating tumours and other
XX proliferative diseases, also for diagnosis
XX Claim 9; Page 59; 76pp; English.
XX This sequence is a novel peptide nucleic acid (PNA), which acts as
XX an inhibitor of telomerase. The PNA is designed to specifically
XX hybridise specifically to an RNA component of mammalian telomerase,
XX and include the sequence GGG for specific hybridisation to the template
XX region of this component. PNAs can be used as probes to detect the
XX activity of telomerase in cells and tissues. Inhibitors of telomerase
XX activity, especially in the treatment of cancer.
XX Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;
SU Query Match 100.0%; Score 6; DB 18; Length 9;
Query Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGG 6
2 TTACGG 8

Db

Search completed: December 31, 2003, 15:08:16
Job time : 173.392 secs

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inflammation; lymphoproliferative disease; autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.

XX Homo sapiens.

XX Synthetic.

XX Key

XX Location/Qualifiers

XX modified base 1..8

XX /note= "this sequence is a peptide nucleic acid, i.e. it contains a polyamide backbone instead of a deoxyribose backbone"

XX US6294650-B1.

XX 25-SEP-2001.

XX 08-JUL-1999; 99US-0349532.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1997; 96US-0630015.

XX (TEKA) UNIV TEXAS SYSTEM.

XX Shay JW, Wright WE, Platyszek MA, Corey DR, Norton JC; WPI; 2001-638024/73.

XX New peptide nucleic acids that hybridizes to the RNA component of mammalian telomerase, useful for treating or preventing cancer, or inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases

XX Claim 7; Column 73; 46pp; English.

XX The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian cells by hybridizing to the RNA component of mammalian telomerase. The PNAs are useful as probes to detect the RNA component of telomerase and/or quantitate polynucleotide having the human telomerase RNA component (hTR) sequence, as well as in forensic identification of suspects or unknown descendants based on the hTR gene RFLP. Certain PNAs can be further used for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals such as antineoplastic or cytostatic agents can be used for treating neoplasia, hyperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (AIDS) and associated pathologies, and other diseases. The present sequence represents one of the PNA sequences of the invention.

XX Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

XX Query Match 100.0%; Score 6; DB 23; Length 8;

XX Identical Similarity 100.0%; Pred. No. 3.2e+08; Mismatches 0; Gaps 0;

XX Matches 0; Conservative 0; Mismatches 0; Gaps 0;

XX 1 ITA000 6

XX 2 ITA000 7

XX Db

XX RESULT 13

XX AAS15474

XX ID AAS15474 standard; DNA; 8 BP.

XX AAS15474;

XX 14-FEB-2002 (first entry)

XX PNA 34 inhibiting human and mammalian telomerase activity.

XX NM Human; peptide nucleic acid; probe; forensic; paternally testing; human telomerase RNA component; hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease; autoimmune disease; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.

XX Homo sapiens.

XX Synthetic.

XX Key

XX Location/Qualifiers

XX modified base 1..8

XX /tag= a

XX /note= "this sequence is a peptide nucleic acid, i.e. it contains a polyamide backbone instead of a deoxyribose backbone"

XX modified base 1..8

XX /tag= b

XX /note= N= 1-50 peptide nucleic acid nucleobases, selected from U, T, A, G, C or i*

XX modified base 9..18

XX /tag= c

XX /note= N= 1-50 peptide nucleic acid nucleobases, selected from U, T, A, G, C or i*

XX US6294650-B1.

XX 25-SEP-2001.

XX 08-JUL-1999; 99US-0349532.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1997; 96US-0630015.

XX (TEKA) UNIV TEXAS SYSTEM.

XX Shay JW, Wright WE, Platyszek MA, Corey DR, Norton JC; WPI; 2001-638024/73.

XX New peptide nucleic acids that hybridizes to the RNA component of mammalian telomerase, useful for treating or preventing cancer, or inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases

XX Disclosure; Column 59; 46pp; English.

XX The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian cells by hybridizing to the RNA component of mammalian telomerase. The PNAs are useful as probes to detect the RNA component of telomerase and/or quantitate polynucleotide having the human telomerase RNA component (hTR) sequence, as well as in forensic identification of individuals, such as paternally testing or identification of criminal suspects or unknown descendants based on the hTR gene RFLP. Certain PNAs can be further used for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals such as antineoplastic or cytostatic agents can be used for treating neoplasia, hyperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (AIDS) and associated pathologies, and other diseases. The present sequence represents one of the PNA sequences of the invention.

XX Note: The present sequence is given in the SEQ ID listing but is not mentioned elsewhere in the patent.

Copied from 09980559 on 05/19/2007

XX epithelial cell proliferation, described in the method of the invention.

CC Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

CC Query Match 100.0%; Score 6; DB 23; Length 6;

CC Best Local Similarity 100.0%; Pred. No. 4,3e+08; Indels 0; Gaps 0;

CC Matches 6; Conservative 0; Mismatches 0; Mismatches 0;

CC 1 TTAGGG 6

CC 1 TTAGGG 6

CC RESULT 4

CC AAS14916/G

CC AAS14916/G

CC AAS14916; standard; DNA; 6 BP.

CC 14-FEB-2002 (first entry)

CC Melanin; melanogenic; oligomer; cytotoxic; anti-allergic; ps3;

CC anti-inflammation; DNA repair; proliferation inhibitor; anti-psoriasis;

CC immunosuppressive; dermatological; ophthalmological; anti-psoriasis;

CC immunosuppressive; dermatological; ophthalmological; anti-psoriasis;

CC carcinoma; oxidative stress; hyperproliferative disease;

CC conjunctivitis; allergic rhinitis; vitiligo; as

CC Synthetic.

CC WO200174342-A2.

CC 11-OCT-2001.

CC 30-MAR-2001; 2001WO-US10162.

CC 31-MAR-2000; 2000US-054043.

CC (WFO-) UNIV BOSTON.

CC Gilchrist BA, Year M, Eller M;

CC WPI; 2001-026338/72.

CC Inhibiting proliferation of epithelial cells, useful e.g. for treating

CC carcinoma, using specific oligonucleotides that mimic the effects of

CC ultra-violet light -

CC Claim 1; Page 37; 7app; English.

CC The invention describes inhibition of mammalian epithelial cell

CC its fragment. The compounds, which have cytotoxic, anti-allergic,

CC anti-inflammation, dermatological, ophthalmological, anti-psoriasis,

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CC

CC sequence is melanogenesis associated oligonucleotide #12, the reverse

CC complementary sequence of AAS14901, the reverse of the sequence

CC representing the telomere over-hang sequence (AAS14901), described in the

CC method of the invention.

CC Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 other;

CC Query Match 100.0%; Score 6; DB 23; Length 6;

CC Best Local Similarity 100.0%; Pred. No. 4,3e+08; Indels 0; Gaps 0;

CC Matches 6; Conservative 0; Mismatches 0; Mismatches 0;

CC 1 TTAGGG 6

CC 6 TTAGGG 1

CC RESULT 5

CC AAS14916/G

CC AAS14916; standard; cDNA; 6 BP.

CC 14-FEB-2002 (first entry)

CC Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.

CC Bovine; Bos taurus; EST; expressed sequence tag; totipotence;

CC development; gene; as.

CC Bos taurus.

CC WO200194550-A2.

CC 13-DEC-2001.

CC 07-JUN-2001; 2001WO-US18576.

CC 07-JUN-2000; 2000US-208974P.

CC 06-JUN-2001; 2001US-0876143.

CC (INFI-) INFIGEN INC.

CC Eliarten KJ, Pfister-Ganskow M, Childs L;

CC WPI; 2002-351289/38.

CC An expressed sequence tag (EST), the expression of which, or its

CC complementary sequence, in a cell identifies the cell as a

CC developmentally competent or incompetent cell -

CC Example 16; Page 210, 584pp; English.

CC The present invention describes an expressed sequence tag (EST), where

CC representing all or part of a gene, the expression of which, or its

CC complementary sequence, in a cell identifies the cell as a

CC developmentally competent or incompetent cell. Molecules which induce

CC totipotence in one or more cells. Molecules which induce developmental

CC incompetence in a cell line are useful for preventing a full term

CC pregnancy in an animal and inhibiting totipotence. The molecules are

CC used to prevent the development of a full term pregnancy in an animal of

CC one or more cells of the animal into a specific cell type. The

CC present sequence represents a bovine EST which is given in the

CC simplification of the present invention.

CC Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

CC Query Match 100.0%; Score 6; DB 24; Length 6;

CC Best Local Similarity 100.0%; Pred. No. 4,3e+08; Indels 0; Gaps 0;

CC Matches 6; Conservative 0; Mismatches 0; Mismatches 0;

CC 1 TTAGGG 6

CC 1 TTAGGG 6

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2101872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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SIMMAB129

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ALIGNMENTS

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REFERENCE Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts from 92 31-MAY-2001.
JOURNAL The Johns Hopkins University (US)
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Qy 1 TTAGGG 6
Db 2 TTAGGG 7

RESULT 13
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DEFINITION Sequence 1297 from Patent WO0138577.
ACCESSION AX153381
VERSION AX153381.1 GI:14535032
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts from 92 31-MAY-2001.
JOURNAL The Johns Hopkins University (US)
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Matches 6; Conservative 0; Mismatches 0;
Qy 1 TTAGGG 6
Db 8 TTAGGG 3

RESULT 14
LOCUS AX153382 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1297 from Patent WO0138577.
ACCESSION AX153382
VERSION AX153382.1 GI:14535033
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts from 92 31-MAY-2001.
JOURNAL The Johns Hopkins University (US)
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Qy 1 TTAGGG 6
Db 8 TTAGGG 3

Search completed: December 31, 2003, 17:09:51
Job time : 355.38 secs

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REFERENCE Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts from 92 31-MAY-2001.
JOURNAL The Johns Hopkins University (US)
FEATURES
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    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
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Matches 6; Conservative 0; Mismatches 0;
Qy 1 TTAGGG 6
Db 8 TTAGGG 3

RESULT 15
LOCUS AX153383 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1298 from Patent WO0138577.
ACCESSION AX153383
VERSION AX153383.1 GI:14535034
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts from 92 31-MAY-2001.
JOURNAL The Johns Hopkins University (US)
FEATURES
    source
    1..10 Homo sapiens
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
BASE COUNT 5 a 3 c 0 g 2 t
ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
Qy 1 TTAGGG 6
Db 8 TTAGGG 3

Search completed: December 31, 2003, 17:09:51
Job time : 355.38 secs

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CC /note= 'N=1-50 peptide nucleic acid nucleobases, selected from U, I, A, G, i or C'. Location/Qualifiers

PH Key modified base 8

PT modified base 8

FEATURES

source

1..8 name="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT

1 a 0 c 3 g 2 t 2 others

Query Match

Local Similarity 100.0%; Score 6; DB 6; Length 8;

Best Local 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches

1 TTAGGG 6

2 TTAGGG 7

RESULT 9

LOCUS BD071050 9 bp DNA linear PAT 27-AUG-2002

DEFINITION Modification of mammalian telomerase by peptide nucleic acids.

ACCESSION BD071050.1 GI:22616653

VERSION JP 2001517929-A/16.

KEYWORDS unclassified.

SOURCE UNCLASSIFIED

ORGANISM unclassified.

REFERENCE

1 (bases 1 to 9)

Wasylyuk, M., Wright, M.E., Platysek, M.A., Corey, D. and Morton, J.C.

Wasylyuk, M., Wright, M.E., Platysek, M.A., Corey, D. and Morton, J.C.

TITLES

JOURNAL Patent: JP 2001517929-A 16 09-OCT-2001; Peptide nucleic acids

GERON CORP

INVENTOR

PN JP 2001517929-A/16

PD 09-OCT-2001

PF 09-APR-1997 JP 1997536493

PI JERRY M SHAW, WOODRING E WRIGHT, MICKEYSLAW A PIATYSZEK, DAVID

PI COREY, D

PC CYPK14/00 J61K18/16 C12Q/68

CC Strandedness: single;

CC Topology: linear;

CC /description: Linear; phosphate

CC linkages are replaced by N-(2-aminoethylglycine units linked to nucleobases via glycine amino N through a CC methyleneacetyl linker

PH Key Location/Qualifiers

PT source /organism="unidentified"

1..9 /organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT

2 a 0 c 4 g 3 t

Query Match

Local Similarity 100.0%; Score 6; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.5e+09;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTAGGG 6

3 TTAGGG 8

Db

CC /note= 'N=1-50 peptide nucleic acid nucleobases, selected from U, I, A, G, i or C'. Location/Qualifiers

PH Key modified base 8

PT modified base 8

FEATURES

source

1..8 name="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT

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Query Match

Local Similarity 100.0%; Score 6; DB 6; Length 10;

Best Local 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches

1 TTAGGG 6

2 TTAGGG 7

RESULT 10

LOCUS AR026485 10 bp DNA linear PAT 29-SEP-1999

DEFINITION Rapid and sensitive assay for detecting and distinguishing between. protein kinase C and protein kinase A kinase activities

ACCESSION AR026485

VERSION AR026485.1 GI:5937325

KEYWORDS unclassified.

SOURCE UNCLASSIFIED

ORGANISM UNCLASSIFIED

REFERENCE

1 (bases 1 to 10)

Windle, B.A., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.

Windle, B.A., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.

TITLES

JOURNAL Patent: US 585096-A 10 05-JUN-1999;

FEATURES

source

1..10 /organism="unknown"

BASE COUNT

2 a 0 c 4 g 4 t

Query Match

Local Similarity 100.0%; Score 6; DB 6; Length 10;

Best Local 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches

Oy 1 TTAGGG 6

Db 1 TTAGGG 6

RESULT 11

LOCUS AR243501 10 bp DNA linear PAT 20-DEC-2002

DEFINITION Rapid and sensitive assay for detecting and distinguishing between. protein kinase C and protein kinase A kinase activities

ACCESSION AR243501

VERSION AR243501.1 GI:27290712

KEYWORDS unclassified.

SOURCE UNCLASSIFIED

ORGANISM UNCLASSIFIED

REFERENCE

1 (bases 1 to 10)

Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Andrews, W.H.

Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Andrews, W.H.

TITLES

JOURNAL Patent: US 4475789-A 294 05-NOV-2002;

FEATURES

source

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BASE COUNT

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Query Match

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Best Local 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches

Oy 1 TTAGGG 6

Db 1 TTAGGG 6

RESULT 12

LOCUS AX152177 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 92 from Patent WO0118577.

ACCESSION AX152177

VERSION AX152177.1 GI:14533828

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE

1 (bases 1 to 10)

Shkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

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Qy 1 TTAGGG 6
Db 6 TTAGGG 1

RESULT 6
BD071049
DEFINITION      8 bp      DNA      linear      PAT 27-AUG-2002
Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION      BD071049.1 GI:22616652
VERSION        BD071049.1
KEYWORDS       unclassified
SOURCE         'ORGANISM'
ORGANISM       unclassified
REFERENCE      (bases 1 to 8)
AUTHORS       Shay,J.W., Wright,W.E., Piattyszek,M.A., Corey,D. and Norton,J.C.
TITLE         Modulation of mammalian telomerase by peptide nucleic acids.
JOURNAL       Patent: JP 2001517929-A 15 09-OCT-2001;
COMMENT       OS Unidentified
PN JP 2001517929-A/15
PD 09-OCT-2001
PF 09-OCT-1997 JP 1997536487
PR 05-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
PT COREY,
P1 JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
CC Strandedness: Single;
CC /desc = "peptide nucleic acid (PNA), where (deoxy/ribose- CC
phosphate
CC linkages are replaced by N-(2-aminoethyl)glycine units linked
CC nucleotide bases via glycine amino N through a CC
methylenecarbonyl linker".
FEATURES       Location/Qualifiers
FT source      1..8
FT source      /organism="Unidentified".
FT source      /mol_type="genomic DNA"
FT source      /db_xref="taxon:32644"
FT source      3 a 4 c 0 g 1 t
BASE COUNT    3 a 4 c 0 g 1 t
Query Match    100.0%; Score 6; DB 6; Length 8;
Best Local Similarity 100.0%; Pred No.5:1e+09;
Matches        6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 7 TTAGGG 2

RESULT 8
BD071067
DEFINITION      8 bp      DNA      linear      PAT 27-AUG-2002
Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION      BD071067.1 GI:22616670
VERSION        BD071067.1
KEYWORDS       unclassified
SOURCE         'ORGANISM'
ORGANISM       unclassified
REFERENCE      (bases 1 to 8)
AUTHORS       Shay,J.W., Wright,W.E., Piattyszek,M.A., Corey,D. and Norton,J.C.
TITLE         Modulation of mammalian telomerase by peptide nucleic acids.
JOURNAL       Patent: JP 2001517929-A 33 09-OCT-2001;
COMMENT       OS Unidentified
PN JP 2001517929-A/33
PD 09-OCT-2001
PF 09-APR-1997 JP 1997536487
PR 05-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
PT COREY,
P1 JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
CC Strandedness: Single;
CC /desc = "peptide nucleic acid (PNA), where (deoxy/ribose- CC
phosphate
CC linkages are replaced by N-(2-aminoethyl)glycine units linked
CC nucleotide bases via glycine amino N through a CC
methylenecarbonyl linker".
FEATURES       Location/Qualifiers
FT source      1..8
FT source      /organism="Unidentified".
FT source      /mol_type="genomic DNA"
FT source      /db_xref="taxon:32644"
FT source      3 a 4 c 0 g 1 t
BASE COUNT    3 a 4 c 0 g 1 t
Query Match    100.0%; Score 6; DB 6; Length 8;
Best Local Similarity 100.0%; Pred No.5:1e+09;
Matches        6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 2 TTAGGG 7

RESULT 7
BD071063/c
LOCUS          8 bp      DNA      linear      PAT 27-AUG-2002
Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION      BD071063.1 GI:22616666
VERSION        BD071063.1
KEYWORDS       unclassified
SOURCE         'ORGANISM'
ORGANISM       unclassified
REFERENCE      (bases 1 to 8)
AUTHORS       Shay,J.W., Wright,W.E., Piattyszek,M.A., Corey,D. and Norton,J.C.
TITLE         Modulation of mammalian telomerase by peptide nucleic acids.
JOURNAL       Patent: JP 2001517929-A 29 09-OCT-2001;
COMMENT       OS Unidentified
PN JP 2001517929-A/29
PD 09-OCT-2001
PF 09-APR-1997 JP 1997536487
PR 05-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
PT COREY,
P1 JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
CC Strandedness: Single;
CC /desc = "peptide nucleic acid (PNA), where (deoxy/ribose- CC
phosphate
CC linkages are replaced by N-(2-aminoethyl)glycine units linked
CC nucleotide bases via glycine amino N through a CC
methylenecarbonyl linker".
FEATURES       Location/Qualifiers
FT source      1..8
FT source      /organism="Unidentified".
FT source      /mol_type="genomic DNA"
FT source      /db_xref="taxon:32644"
FT source      1 a 0 c 4 g 3 t
BASE COUNT    1 a 0 c 4 g 3 t
Query Match    100.0%; Score 6; DB 6; Length 8;
Best Local Similarity 100.0%; Pred No.5:1e+09;
Matches        6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 2 TTAGGG 7

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        /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 6.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
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Db

RESULT 2
LOCUS       AX058275                6 bp          DNA          PAT 17-JAN-2001
DEFINITION  Sequence 10 from Patent WO0074667.
ACCESSION   AX058275
VERSION     AX058275.1 GI:12310774
KEYWORDS    synthetic construct
SOURCE      GenBank
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 6)
            Au J.T. and Mont-Joyer G.
            Telomerase inhibitor
            Telomerase inhibitor
            Patent: WO 0074667-A 10 14-DEC-2000;
            Au, Josselin, Mont-Joyer, Guilleume (US)
FEATURES    Location/Qualifiers
            source
                1..6
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                /note="primer/probe"
BASE COUNT      1 a 0 c 3 g          2 t
ORIGIN
Query Match      100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
1 TTTGGG 6

RESULT 3
LOCUS       AX175285                6 bp          DNA          PAT 03-JUL-2001
DEFINITION  Sequence 49 from Patent WO014465.
ACCESSION   AX175285
VERSION     AX175285.1 GI:14598653
KEYWORDS    synthetic construct
SOURCE      GenBank
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 6)
            Gilman M. C.
            Therapeutically useful synthetic oligonucleotides
            Patent: WO 014465-A 49 21-JUN-2001;
            Bioniche Life Sciences Inc. (CA)
FEATURES    Location/Qualifiers
            source
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CANCER INSTITUTE, INC. (US)
FEATURES
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        /note="synthetic primer"
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Best Local Similarity 100.0%; Pred. No. 6.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
        6 TTTGGG 1

Db

RESULT 4
LOCUS       AX268763                6 bp          DNA          PAT 29-OCT-2001
DEFINITION  Sequence 11 from Patent WO0174342.
ACCESSION   AX268763
VERSION     AX268763.1 GI:16541835
KEYWORDS    synthetic construct
SOURCE      GenBank
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 6)
            Gilchrist B.A., Yarr M. and Ellis M.
            Use of locally applied dna fragments
            Patent: WO 0174342-A 11 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES    Location/Qualifiers
            source
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                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                /note="Synthetic DNA Fragment"
BASE COUNT      1 a 0 c 3 g          2 t
ORIGIN
Query Match      100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
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Db

RESULT 5
LOCUS       AX268764                6 bp          DNA          PAT 29-OCT-2001
DEFINITION  Sequence 12 from Patent WO0174342.
ACCESSION   AX268764
VERSION     AX268764.1 GI:16541836
KEYWORDS    synthetic construct
SOURCE      GenBank
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 6)
            Gilchrist B.A., Yarr M. and Ellis M.
            Use of locally applied dna fragments
            Patent: WO 0174342-A 12 11-OCT-2001;
            TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES    Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                /note="Synthetic DNA Fragment"
BASE COUNT      2 a 3 c 0 g          1 t
ORIGIN
Query Match      100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTAGGG 6
        1 TTTGGG 6

Db

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GenCore version 5.1.6

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OW nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 543.38 Seconds
444.364 Million cell updates/sec

Title: US-09-540-843-11
Perfect score: 6
Sequence: 1 tttggtg 6

Scoring table: IDENTITY, NUC
Gapop 10.0, Gapext 1.0

Searched: 288711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 30
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database:

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2: gp-hg*

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27: gp-hg*

28: gp-hg*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	6	100.0	6	AX058275	AX058275 Sequence
C 3	6	100.0	6	AX15285	AX15285 Sequence
C 4	6	100.0	6	AX268763	AX268763 Sequence
C 5	6	100.0	6	AX058275	AX058275 Sequence
C 6	6	100.0	8	BD071049	BD071049 Modulation
C 7	6	100.0	8	BD071063	BD071063 Modulation
C 8	6	100.0	9	BD071067	BD071067 Modulation
C 9	6	100.0	9	BD071067	BD071067 Modulation
C 10	6	100.0	10	AR026485	AR026485 Sequence
C 11	6	100.0	10	AR243501	AR243501 Sequence
C 12	6	100.0	10	AX153382	AX153382 Sequence
C 13	6	100.0	10	AX153382	AX153382 Sequence
C 14	6	100.0	10	AX153382	AX153382 Sequence
C 15	6	100.0	10	AX153382	AX153382 Sequence
C 16	6	100.0	10	AX153382	AX153382 Sequence
C 17	6	100.0	10	BD011231	BD011231 Human tel
C 18	6	100.0	10	BD033724	BD033724 Method fo
C 19	6	100.0	10	BD071049	BD071049 Modulation
C 20	6	100.0	10	BD071049	BD071049 Modulation
C 21	6	100.0	10	BD071051	BD071051 Modulation
C 22	6	100.0	10	BD071054	BD071054 Modulation
C 23	6	100.0	10	BD071054	BD071054 Modulation
C 24	6	100.0	10	BD167218	BD167218 Modulation
C 25	6	100.0	10	E3680	E3680 Human telom
C 26	6	100.0	11	AR016034	AR016034 Sequence
C 27	6	100.0	11	AR026487	AR026487 Sequence
C 28	6	100.0	11	AR026487	AR026487 Sequence
C 29	6	100.0	11	AR059195	AR059195 Sequence
C 30	6	100.0	11	AR075506	AR075506 Sequence
C 31	6	100.0	11	AR151804	AR151804 Sequence
C 32	6	100.0	11	AR214804	AR214804 Sequence
C 33	6	100.0	11	AR301476	AR301476 Sequence
C 34	6	100.0	11	AR301690	AR301690 Sequence
C 35	6	100.0	11	AR303373	AR303373 Sequence
C 36	6	100.0	11	AX033373	AX033373 Sequence
C 37	6	100.0	11	AX268757	AX268757 Sequence
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ALIGNMENTS

RESULT 1	AX058601/c	AX058601	6 bp	DNA	linear	PAT 13-JAN-2001
DEFINITION	AX058601	5	From Patent WO0073420.			
VERSION	AX058601	1	GI:12228914			
ACCESSION	AX058601	1	GI:12228914			
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	artificial sequences					
REFERENCE	artificial sequences					
AUTHORS	Hahn, W.C. and Weinberg, R.A.					
TITLE	Creation of human tumorigenic cells and uses therefor					
JOURNAL	Parent: WO 0073420-A 5 07-DEC-2000					
	WILHELM INSTITUTE FOR MEDICAL RESEARCH (US) ; DNA-PARBER					

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Search completed: January 1, 2004, 01:10:39
Job time : 234.165 secs

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RESULT 14
US-10-408-736-66/c
; Sequence 66, Application US/10408736
; Patent Information: US/03030175508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Hwang, Jung-Shong
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-Young
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US P1
; CURRENT APPLICATION NUMBER: US/10408736
; PRIOR APPLICATION NUMBER: US/09379095A
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FUNCTION: Primer
; OTHER INFORMATION: Reverse Primer R0352
US-10-408-736-66
Query Match 50 04; Score 11.9; DB 13; Length 18;
Best Local Similarity 86.7%; Read No. 2; 4e+01;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 CGCGCATCTTACGACG 20
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18 CAGCGCTTACGACG 4

RESULT 15
US-09-540-185-3327
; Sequence 327, Application US/09540185
; Patent Information: US/0303096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09540185
; PRIOR APPLICATION NUMBER: US/0227948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3327
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FUNCTION: Probe
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-540-185-3327
Query Match 50 04; Score 11.9; DB 11; Length 24;
Best Local Similarity 86.7%; Read No. 2; 4e+01;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CGATGATCGATTCAC 15
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8 CGATGATCGCTTCG 22

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Db          9 GCGGGGCTTCGCTGACCT 25

RESULT 10
US-10-230-562-43
  APPLICANT: Leonard, Amanda Run-yeong
  APPLICANT: Huang, Yung-Sheng
  APPLICANT: Pereira, Susette L.
  TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
  PUBLICATION NO. US2003013886A1
  CURRENT FILING DATE: 2003-07-11
  CURRENT APPLICATION NUMBER: US/09/503,456
  PRIOR APPLICATION NUMBER: US 09/624,670
  PRIOR FILING DATE: 2001-07-11
  PRIOR APPLICATION NUMBER: US 09/379,095
  PRIOR FILING DATE: 1999-08-23
  PRIOR APPLICATION NUMBER: US 09/145,928
  PRIOR FILING DATE: 1998-09-02
  NUMBER OF SEQ ID NOS: 116
  SOFTWARE: FastSeq for Windows Version 4.0
  LENGTH: 18
  TYPE: DNA
  ORGANISM: Artificial Sequence
  OTHER INFORMATION: Reverse Primer R0352
US-09-903-456-93
  Query Match          59.0%; Score 11.8; DB 10; Length 18;
  Best Local Similarity 86.7%; Pred. No. 2.4e+04;
  Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          6 CAGCATGCTAGCTAGC 20
Db          18 CAGGCTTTAGCTAGC 4

RESULT 13
US-10-156-911-93/c
  APPLICANT: Leonard, Amanda Run-yeong
  APPLICANT: Huang, Yung-Sheng
  APPLICANT: Pereira, Susette L.
  TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
  PUBLICATION NO. US2003013845A1
  CURRENT FILING DATE: 2001-07-11
  CURRENT APPLICATION NUMBER: US/10/156-911
  PRIOR APPLICATION NUMBER: US 09/624,670
  PRIOR FILING DATE: 2001-07-11
  PRIOR APPLICATION NUMBER: US 09/379,095
  PRIOR FILING DATE: 1999-08-23
  PRIOR APPLICATION NUMBER: US 09/145,928
  PRIOR FILING DATE: 1998-09-02
  NUMBER OF SEQ ID NOS: 122
  SOFTWARE: FastSeq for Windows Version 4.0
  LENGTH: 18
  TYPE: DNA
  ORGANISM: Artificial Sequence
  OTHER INFORMATION: Reverse Primer R0352
US-10-156-911-93
  Query Match          59.0%; Score 11.8; DB 13; Length 18;
  Best Local Similarity 86.7%; Pred. No. 2.4e+04;
  Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          6 CAGCATGCTAGCTAGC 20
Db          18 CAGGCTTTAGCTAGC 4

US-10-098-263B-31016
  APPLICANT: Human Microarray
  TITLE OF INVENTION: Human Microarray
  PUBLICATION NO. US2003010410A1
  CURRENT FILING DATE: 2003-01-06
  CURRENT APPLICATION NUMBER: 60/276,759
  PRIOR FILING DATE: 2001-03-16
  PRIOR APPLICATION NUMBER: US/10/098,263B
  SOFTWARE: Microarray Probe Sequence Liasing Generator v 1.1
  SEQ ID NO 31016
  LENGTH: 25
  ORGANISM: Homo sapien
US-10-098-263B-31016
  Query Match          60.0%; Score 12; DB 15; Length 25;
  Best Local Similarity 75.0%; Pred. No. 2e+04;
  Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy          1 GCGATGATGCTAGCTAGC 20
Db          3 GCGATGATGCTAGCTAGCTCG 22

RESULT 12
US-09-903-456-93/c
  APPLICANT: Leonard, Amanda Run-yeong
  APPLICANT: Huang, Yung-Sheng
  APPLICANT: Pereira, Susette L.
  TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
  PUBLICATION NO. US2003013887A1
  CURRENT FILING DATE: 2003-07-11
  CURRENT APPLICATION NUMBER: US/09/903,456
  PRIOR APPLICATION NUMBER: US 09/624,670
  PRIOR FILING DATE: 2001-07-11
  PRIOR APPLICATION NUMBER: US 09/379,095
  PRIOR FILING DATE: 1999-08-23
  PRIOR APPLICATION NUMBER: US 09/145,928
  PRIOR FILING DATE: 1998-09-02
  NUMBER OF SEQ ID NOS: 116
  SOFTWARE: FastSeq for Windows Version 4.0
  LENGTH: 18
  TYPE: DNA
  ORGANISM: Artificial Sequence
  OTHER INFORMATION: Reverse Primer R0352
US-09-903-456-93
  Query Match          59.0%; Score 11.8; DB 13; Length 18;
  Best Local Similarity 86.7%; Pred. No. 2.4e+04;
  Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          6 CAGCATGCTAGCTAGC 20
Db          18 CAGGCTTTAGCTAGC 4

```

DB 17 ATCGTCGATGTCATC 1

RESULT 6
US-10-245-805-20/C
Sequence 20, Application US/10245805
Best Local Similarity 82.4%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: GRAMM, Michael Wayne
APPLICANT: RICE, Robert No. US20030182672Alan
APPLICANT: MURPHY, Kathleen Margaret
APPLICANT: MURPHY, Kathleen Margaret
APPLICANT: Benitec Australia Ltd
APPLICANT: The State of Queensland through its Department of Primary Industries
FILE REFERENCE: 5463220020
CURRENT APPLICATION NUMBER: US/10/245, 805
CURRENT FILING DATE: 2002-07-16
PRIOR FILING DATE: 2001-03-16 AU/1/00297
PRIOR APPLICATION NUMBER: AU P06363
PRIOR APPLICATION NUMBER: AU P06363
PRIOR APPLICATION NUMBER: AU PR2700
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 20: FastSeq for Windows Version 4.0
LENGTH: 23
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Double Stranded DNA Probe
US-10-245-805-20

Query Match 61.0%; Score 12.2; DB 13; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATCGTCGATGTCATC 19
DB 20 ATCGTCGATGTCATC 4

RESULT 7
US-10-245-805-21/C
Sequence 21, Application US/10245805
Publication No. US20030182672Alan
GENERAL INFORMATION:
APPLICANT: GRAMM, Michael Wayne
APPLICANT: RICE, Robert No. US20030182672Alan
APPLICANT: MURPHY, Kathleen Margaret
APPLICANT: MURPHY, Kathleen Margaret
APPLICANT: Benitec Australia Ltd
APPLICANT: The State of Queensland through its Department of Primary Industries
FILE REFERENCE: 5463220020
CURRENT APPLICATION NUMBER: US/10/245, 805
CURRENT FILING DATE: 2002-07-16
PRIOR FILING DATE: 2001-03-16 AU/1/00297
PRIOR APPLICATION NUMBER: AU P06363
PRIOR APPLICATION NUMBER: AU P06363
PRIOR APPLICATION NUMBER: AU PR2700
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 21: FastSeq for Windows Version 4.0
LENGTH: 23
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Double Stranded DNA Probe
US-10-245-805-21

Query Match 61.0%; Score 12.2; DB 13; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATCGTCGATGTCATC 19
DB 20 ATCGTCGATGTCATC 4

US-10-245-805-21

Query Match 61.0%; Score 12.2; DB 13; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATCGTCGATGTCATC 19
DB 20 ATCGTCGATGTCATC 4

RESULT 8
US-09-540-185-2034/C
Sequence 2034, Application US/09940185
Publication No. US20030094239Al
GENERAL INFORMATION:
APPLICANT: Chae, Mark
APPLICANT: Chae, Mark
TITLE OF INVENTION: Probes and Decoder Oligonucleotides
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 4768
NUMBER OF SEQ ID NOS: 4768
SEQ ID NO 2034
LENGTH: 24
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-540-185-2034

Query Match 61.0%; Score 12.2; DB 11; Length 24;
Best Local Similarity 82.4%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TCGATCGATGTCATCG 20
DB 22 TCGATCGATGTCATCG 6

RESULT 9
US-09-540-314-43
Sequence 43, Application US/09954314
Patent No. US20020127666Al
GENERAL INFORMATION:
APPLICANT: Brzostowski, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
CURRENT APPLICATION NUMBER: US 09/954,314
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 49
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 43
LENGTH: 43
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-540-314-43

Query Match 61.0%; Score 12.2; DB 10; Length 30;
Best Local Similarity 82.4%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGATCGATGTCATCG 17

```

Db      1  GCATCATGCATGATGAC 20
|||||
RESULT 2
US-10-122-633-8
Sequence 8, Application US/1012633
Publication No. US2003003261A1
APPLICANT: Glitcher, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Oligonucleotide
FILE REFERENCE: 0054-1088-019
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
PRIMER: Synthetic DNA Fragment
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-8
Query Match 100.0%; Score 20, DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  GCATCATGCATGATGAC 20
|||||
1  GCATCATGCATGATGAC 20
|||||
RESULT 3
US-10-194-035-45/2
Sequence 95, Application US/10194035
Publication No. US2003014229A1
APPLICANT: KLINMAN, Dennis
APPLICANT: KLINMAN, Dennis
TITLE OF INVENTION: OLIGONUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10194.035
PRIOR APPLICATION NUMBER: PCT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 1994-03-16
NUMBER OF SEQ ID NOS: 119
SOFTWARE: patentin Ver. 2.1
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-95
Query Match 65.0%; Score 13, DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 66.03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  GCATCATGCATG 13
|||||

```

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Db      13  GCATCATGCATG 11
|||||
RESULT 4
US-09-232-785-139
Sequence 139, Application US/09232785
Publication No. US20030049612A1
APPLICANT: International Paper Co.
APPLICANT: Echt, Craig S.
TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
FILE REFERENCE: 4481/1818001/09/232.785
CURRENT FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: 09/232.884
PRIOR FILING DATE: 1999-01-15
SOFTWARE: FastSeq for Windows Version 3.0
LENGTH: 20
TYPE: DNA
ORGANISM: Pinus taeda L.
US-09-232-785-139
Query Match 61.0%; Score 12.2; DB 11; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4  TCATCATGCATGAC 20
|||||
Db      1  TCATCATGCATGAC 17
|||||
RESULT 5
US-10-079-489-31/5
Sequence 31, Application US/10079429
Publication No. US2003002177A1
GENERAL INFORMATION:
TITLE OF INVENTION: Human DNA Mismatch Repair Process
FILE REFERENCE: PF106P3D1
CURRENT APPLICATION NUMBER: US/10/079.429
PRIOR APPLICATION NUMBER: PCT/US95/01035
PRIOR FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 08/468.024
PRIOR APPLICATION NUMBER: 08/465.769
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 09/294.312
PRIOR APPLICATION NUMBER: 08/210.113
PRIOR FILING DATE: 1994-03-16
PRIOR APPLICATION NUMBER: 09/187.757
NUMBER OF SEQ ID NOS: 78
SOFTWARE: patentin version 3.0
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: MUSH sense primer
US-10-079-429-21
Query Match 61.0%; Score 12.2; DB 15; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3  ATCATCATGATGAC 19
|||||

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GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00, Search time 233.165 Seconds
296.896 Million cell updates/sec

File: US-09-540-843-8
Perfect score: 20
Sequence: 1 gcatcgctgcatgctagc 20

Scoring table: IDENTITY: 100
Gapop 10.0, Gapext 1.0

Searched: 226343 seqs, 1730637950 residues
Total number of hits satisfying chosen parameters: 999502

Minimum seq length: 0
Maximum seq length: 30

Post-processing: Minimum Match 0
Minimum Match 45
Largest hit 15 summaries

Database: Published Applications N.A.
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13. /cgm2_6/pdataa1/pubna/US06_PUBCOMB.seq.
14. /cgm2_6/pdataa1/pubna/US06_PUBCOMB.seq.
15. /cgm2_6/pdataa1/pubna/US06_PUBCOMB.seq.
16. /cgm2_6/pdataa1/pubna/US06_PUBCOMB.seq.
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18. /cgm2_6/pdataa1/pubna/US06_PUBCOMB.seq.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Match	Length	DB	ID	Description
1	20	100.0	20	15	US-10-122-630-8	Sequence 8, Appl
2	20	100.0	20	15	US-10-122-630-8	Sequence 9, Appl
3	20	100.0	20	15	US-10-122-630-8	Sequence 10, Appl
4	12.2	61.0	20	11	US-05-232-705-139	Sequence 139
5	12.2	61.0	20	13	US-10-079-439-21	Sequence 21, Appl
6	12.2	61.0	20	13	US-10-245-805-20	Sequence 20, Appl
7	12.2	61.0	20	13	US-10-245-805-20	Sequence 20, Appl
8	12.2	61.0	20	11	US-05-232-705-139	Sequence 139
9	12.2	61.0	24	11	US-05-940-195-2034	Sequence 2034
10	12.2	61.0	30	10	US-05-954-314-43	Sequence 43, Appl
11	12.2	61.0	30	15	US-10-230-562-43	Sequence 43, Appl
12	11.8	59.0	18	10	US-05-903-456-93	Sequence 93, Appl
13	11.8	59.0	18	13	US-10-156-911-93	Sequence 93, Appl
14	11.8	59.0	18	13	US-10-408-736-66	Sequence 66, Appl
15	11.8	59.0	24	11	US-05-940-195-2034	Sequence 2034, Appl

Sequence 60894, A
Sequence 191, Appl
Sequence 44, Appl
Sequence 3, Appl
Sequence 12, Appl
Sequence 20, Appl
Sequence 21, Appl
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Sequence 10574, A
Sequence 10574, A
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Sequence 93, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 90, Appl

25 15 US-10-098-2638-60894
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20 13 US-10-194-035-90
20 13 US-10-194-035-90

ALIGNMENTS

RESULT 1
US-10-122-630-8
Sequence 8, Application US/10122630
Sequence 8, Application US/10122630
GENERAL INFORMATION: US/10122630:UAI
APPLICANT: Glitchest, Barbara A.
APPLICANT: Glitchest, Barbara A.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
Oligonucleotides
CURRENT FILING DATE: 2004-08-18/10122, 630
PRIORITY FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
SEQ ID NO 9
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-8

Query Match 100.0% Score 20, DB 15, Length 20,
Best Local Similarity 100.0%, Pref No. 231, 0,
Matches 20, Conservative 0, Mismatches 0, Gaps 0,
1 GCGTCGCTGCTAGCTAGC 20

STREET: 633 West Fifth Street
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP CODE: 94102
 COMPUTES READABLE PDBM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM Compatible
 COMPATIBLE SYSTEM: DOS (Version 5.0)
 SOFTWARE: ModPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/724,753
 PENDING NUMBER: US/09-5408
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 PENDING NUMBER: 09/123,638
 FILING DATE: Unknown
 ATTORNEY/AGENT INFORMATION:
 NAME: Kappoe, John
 PENDING NUMBER: 37,861
 REFERENCE/DOCKET NUMBER: 821/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 489-1600
 TELEFAX: (415) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: nucleic acid
 STRANDEDNESS: single
 COMPOSITION: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

us-09-724-753-3

Query Match 58.0%; Score 11.6; De 4; Length 20;
 Query Match Similarity 58.0%; RefSeq 58.0%;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Search completed: January 1, 2004, 00:32:19
 Job time : 77.8326 secs

1 TOPOLOGY: linear
 2 MOLECULE TYPE: DNA (genomic)
 3 HYPOTHETICAL: NO
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 6
 7 Query Match 58.0%; Score 11.6; DB 1; Length 20;
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 9 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 12 Db 20 ATGCATGCACTAGTAG 3
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RESULT 14
 US-09-123-638-3/c
 Sequence 3, Application US/09123638
 GENERAL INFORMATION:
 APPLICANT: Michael J. Heller
 TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTOMIC
 STRUCTURES BASED ON CHROMOPHORE-
 CONTAINING POLYNUCLEOTIDES AND METHODS OF
 THEIR USE
 TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF
 THEIR USE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS: 11
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/123.638
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/703.601
 ATTORNEY/AGENT INFORMATION:
 NAME: Kappos, John
 REGISTRATION NUMBER: 37,861
 REFERENCE/DOCKET NUMBER: 21/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-1510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-123-638-3
 Query Match 58.0%; Score 11.6; DB 3; Length 20;
 Beat Local Similarity 77.8%; Pred. No. 2.8e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 3 ATGCATGCACTAGTAG 20
 Db 20 ATGCATGCACTAGTAG 3
 RESULT 15
 US-09-71-753-3/c
 Sequence 3, Application US/09724753
 GENERAL INFORMATION:
 APPLICANT: Michael J. Heller
 TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTOMIC
 STRUCTURES BASED ON CHROMOPHORE-
 CONTAINING POLYNUCLEOTIDES AND METHODS OF
 THEIR USE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS: 11
 ADDRESSEE: Lyon & Lyon

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: unknown
US-09-134-855-1

Query Match 60.0%; Score 12; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTCGATGATC 12
|||||
DB 13 SCATCGATGATC 2

US-09-145-828A-28/c
Sequence 26; Application US/09145828A
Sequence 40; Artificial Sequence

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

INVENTOR: Richard A. Lerner

APPLICANT: Leonard Asada E. Y.

APPLICANT: Huang, Yung-Sheng

APPLICANT: Thurmond, Jennifer

APPLICANT: Parker-Barnes, Jennifer

TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF

FILE REFERENCE: 6407/US 01 US/09/145, 828A

CURRENT FILING DATE: 1998-09-02

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 28: FastSeq for Windows Version 4.0

LENGTH: 18

TYPE: DNA

FEATURE: Artificial Sequence

OTHER INFORMATION: Primer R0352

US-09-145-828A-28

Query Match 59.0%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 CAGTCGATGATC 20
|||||
18 CAGCTTCGATGATC 4

RESULT 11
Sequence 31; Application US/08250951
Sequence 3; Artificial Sequence

GENERAL INFORMATION:

APPLICANT: Michael J.

TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC

TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING

TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF THEIR USE

NUMBER OF INVENTIONS: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bingham & Fitting

CITY: 1256 High Bluff Drive, Suite 300

STATE: California

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: GENVIEW

CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/250,951

FILING DATE:

CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/790,262

FILING DATE: 07-NOV-1991

APPLICANT: Bingham & Fitting

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: HEL0002P

TELEPHONE: 619-792-3680

TELEFAX: 619-792-8477

INVENTOR: Bingham & Fitting

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

TOPOLOGY: single

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

US-08-230-951-3

Query Match 59.0%; Score 11.6; DB 1; Length 20;

Best Local Similarity 86.7%; Pred. No. 2.2e+03;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATGCAATGATGATGATC 20

DB 20 ATGCAATGATGATGATC 3

RESULT 12

US-08-232-233-3/c

Sequence 3; Application US/08232233

Sequence 3; Artificial Sequence

GENERAL INFORMATION:

APPLICANT: Michael J. Heller

TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC

TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-

TITLE OF INVENTION: CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

COMPUTER: IBM compatible, 1.44 Mb storage

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA: US/08/232,233

FILING DATE: May 4, 1994

APPLICATION NUMBER: US/08/232,233

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/790,262

FILING DATE: No. 5565322 December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Audrey David

REGISTRATION NUMBER: 31,125

REFERENCE/DOCKET NUMBER: 207/170

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INVENTOR: Bingham & Fitting

TELEPHONE: 619-792-3680

INVENTOR: Bingham & Fitting

INVENTOR: Bingham & Fitting

INVENTOR: Bingham & Fitting

INVENTOR: Bingham & Fitting

INVENTOR: Bingham & Fitting

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FEATURE:
OTHER INFORMATION: hmlkl sense primer
US-08-187-797D-19
Query Match 61.0%; Score 12.2; DB 4; Length 21;
Best Local Similarity 82.4%; Prod. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGCTCATCATCTAC 19
Db 18 ATGCTCATCATCTAC 2

RESULT 6
US-09-504-358-43
Sequence 43, Application US/09504358
Patent No. 6465376
APPLICANT: Roviere, Pierre E.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
FILE REFERENCE: BC1001 US NA
CURRENT FILING DATE: 2000-02-15
EARLIER APPLICATION NUMBER: 60/120,702
EARLIER FILING DATE: 1999-February-19
SOFTWARE: Microsoft Office 97
SEQ ID NO 43
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-504-358-43
Query Match 61.0%; Score 12.2; DB 4; Length 30;
Best Local Similarity 82.4%; Prod. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATCATCATCATCT 17
Db 9 GCATCATCATCATCT 25

RESULT 7
US-09-954-314-43
Sequence 43, Application US/09954314
Patent No. 6465224
APPLICANT: Roviere, Pierre E.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
FILE REFERENCE: BC1001 US NA
CURRENT FILING DATE: 2001-09-17
EARLIER APPLICATION NUMBER: 60/120,702
EARLIER FILING DATE: 1999-February-19
SOFTWARE: Microsoft Office 97
SEQ ID NO 43
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-954-314-43
Query Match 61.0%; Score 12.2; DB 4; Length 30;
Best Local Similarity 82.4%; Prod. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATCATCATCATCT 17

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Db 9 GCATCATCATCATCT 25

RESULT 8
US-09-134-855-1
Sequence 1, Application US/09134855
Patent No. 6107038
APPLICANT: CHODURY, Gargi
TITLE OF INVENTION: Method of Binding a Plurality of Chemicals on a Substrate by Electrophoretic Self-Assembly
FILE REFERENCE: 5000050
CURRENT FILING DATE: 1998-08-14
CURRENT APPLICATION NUMBER: US/09/134,855
SOFTWARE: PatcinIn Ver. 2.1
SEQ ID NO 1
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: n is 2: fluorodeoxytyridine
US-09-134-855-1
Query Match 60.0%; Score 12; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 1.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATCATCATCT 12
Db 4 GCATCATCATCT 15

RESULT 9
US-09-134-855-1/c
Sequence 1, Application US/09134855
Patent No. 6107038
APPLICANT: CHODURY, Gargi
TITLE OF INVENTION: Method of Binding a Plurality of Chemicals on a Substrate by Electrophoretic Self-Assembly
FILE REFERENCE: 5000050
CURRENT FILING DATE: 1998-08-14
CURRENT APPLICATION NUMBER: US/09/134,855
SOFTWARE: Seq ID NOS: 5
SEQ ID NO 1
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: n is 2: fluorodeoxytyridine

```


Copied from 09980559 on 05/19/2004

Fax: 801 385 7177
Email: dunn@genetics.utah.edu
Phone: 801 378 1080
Plate: C98H
Seq primer: CACAAGACAAAGATTC
Seq primer: CACAAGACAAAGATTC
Class: Plasmid endon. exp. 26
High qual. data
Location/Qualifiers
1. .36
 name="mus musculus"
 mol_type="genomic DNA"
 strain="C57BL/6j"
 sex="Male"
 clone="U9C:NM039826"
 clone="U9C:NM039826"
 sex="Male"
 lab_host="E. Coli strain XL10"
 method="PCR"
 method="PCR:NM042991"
 musculus="C57BL/6j (male)"
 laboratory="Mouse DNA Resource"
 laboratory="Mouse DNA Resource"
 was_hydrodynamically_sheared="No"
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Query Match      61.0%   Score 12.2   DB 28   Length 26;
Best Local Similarity 82.4%   Pred. No. 9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

          2  CATGCAATGCAATAGTGA 18
Dy         1  | | | | | | | | | |
          21 CATGCAAGCATATATGA 5
Db

RESULT 3
D45819
HMMSEARCH
DEFINITION
D45819 Homo sapiens adult lung 3' , directed MboI cDNA Homo sapiens CDNA
3' , mRNA sequence.
D45819
FEATURES
    accession      D45819
    version        052419.1
    GI             GI:662773
    source         Homo sapiens
    organism       Homo sapiens
    Rukerology     Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Rukerology     Primates; Catarrhini; Hominoidea; Homo.
    Itoh.K.        K. Kubo.K., Yosi.J., Yokouchi.H. and Masubara.K.
    title          An expression profile of active genes in human lung
    title          (base 1 to 29)
    title          (base 1 to 29)
    title          2, 275-287 (1994)
    keywords        95236275
    PUBMED         7719923
    contact        Contact: Kichichi Itoh
    comment        Department of Molecular and Cellular Biology
    comment        Osaka University
    comment        3-1, Yamadaoka, Suita, Osaka, 565, Japan
    comment        Tel. 06-877-5111 X3910
    comment        Fax. 06-877-5111
    comment        Location/Qualifiers
FEATURES

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XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX Bergeron M, Boisjot M, Huletsky A, Menard C, Ouellette M,
 XX Picard FJ, Roy PH;
 XX WPI; 2001-24506/25.
 XX Nucleic acid sequences are used to generate universal probes and
 XX primers which can be used to identify and detect the presence of algal,
 XX archaeal, bacterial, fungal and parasitical species in a test sample -
 XX Claim 21, Page 1456; 1580pp; English.
 XX The present invention describes a method for generating a repertory of
 XX nucleic acids of tumour, viral, bacterial, fungal and parasitical
 XX acids of determined algal, archaeal, bacterial, fungal and parasitical
 XX species with a combination of defined primer pairs. The method can be
 XX used to detect the presence of tumour, viral, bacterial, fungal and
 XX related microorganisms in a sample. The method can be used for
 XX parasitology, for universal detection and for specific and ubiquitous
 XX detection and identification of an algal, archaeal, bacterial, fungal
 XX and parasitical species. The method can be used for the universal
 XX detection using the method of the invention can be used for the universal
 XX detection of any bacterium, fungus or parasite in a sample and for the
 XX detection of at least one antimicrobial agent resistance gene or of an
 XX antimicrobial agent resistance gene. The method can be used for the
 XX ubiquitous detection and for identification of *Streptococcus pneumoniae*.
 XX (1) can be used to design a therapeutic agent which is effective against
 XX the tumour, viral, bacterial, fungal and parasitical species group
 XX which can be detected include *Alotrophia adiscens*, *Bordetella sp.*,
 XX *Corynebacterium sp.*, *Enterobacteriaceae* group, *Escherichia coli*,
 XX *Mycobacteriaceae* family, *Pseudomonade* group, *Streptococcus sp.*,
 XX *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus*
 XX provides faster results than substrate specificity tests as results can
 XX be determined in an hour and improved accuracy is also achieved.
 XX AM00010 to AM002304 represent nucleotide sequences and primers/probes
 XX which are given in the compilation of the present invention.
 XX Sequence 23 BP; 8 A; 6 C; 4 G; 5 T; 0 other;
 XX Query Match 61.0%; Score 12.2; DB 22; Length 23;
 XX Best Local Similarity 82.4%; Pred. No. 8.2e+03;
 XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 2 CATGCTGATCATGCTA 18
 XX |||||
 XX 3 CAGATGCTATATGCA 19
 XX
 XX RESULT 15
 XX AM01113/2
 XX AM01112 standard; DNA; 24 BP.
 XX ABX14112;
 XX 25-FEB-2003 (first entry)
 XX Human zinc finger protein 8.8 specific RT-PCR primer. #2.
 XX Zinc finger protein 8.8; human; RT-PCR; as: tumour; haemopoietic;
 XX human immunodeficiency virus; HIV; immunological disease; inflammation;
 XX antagonist; reverse transcription; primer.
 XX Homo sapiens.
 XX CN132505-A.
 XX 05-JUN-2002.
 XX 02-NOV-2000; 2000CN-0127133.
 XX

02-NOV-2000, 2000CN-0127133.
 (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Mao Y, Xie Y;
 WPI; 2002-64445/70.
 New polypeptide human zinc finger protein 8.8 and polynucleotide for
 encoding such polypeptide -
 Example 2, Page 16 (disclosure); 32pp; Chinese.
 The present invention discloses a novel human zinc finger protein 8.8,
 polynucleotide coding for the polypeptide and method for producing this
 polynucleotide and method for using the polynucleotide, such as malignant
 tumour, haemopathy, human immunodeficiency virus (HIV) infection,
 immunological diseases and various inflammations by using the
 polynucleotide and its therapeutic action and also discloses the
 said polypeptide and its therapeutic action and also discloses the
 application of the polynucleotide for coding this novel zinc finger
 protein 8.8. The sequences presented is the reverse transcription
 primer, #2, which was used to isolate human zinc finger protein
 8.8 cDNA.
 Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other;
 Query Match 61.0%; Score 12.2; DB 24; Length 24;
 Best Local Similarity 82.4%; Pred. No. 8.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GATGCTGATCATGCT 17
 |||||
 DB 20 GCTGCTGATGCTGCT 4

Search completed: December 31, 2003, 15:08:16
 Job time : 576.375 sec

CC Probe #2 (AAQ45657) hybridizes to, and is specific for, the 16S rRNA of
 CC S. typhimurium. Hybridisation was enhanced by the use of "helper probe".
 CC AAQ45971 and AAQ45972. The probe can be used alone or in a mix with
 CC other S. typhimurium-specific probes to distinguish S. typhimurium from
 CC closely related bacteria (i.e. other *Streptococcus* spp.).

XX Sequence 26 BP; 5 A; 6 C; 6 G; 7 T; 0 other;
 Query Match 63.0%; Score 12.6; DB 14; Length 26;
 Best Local Similarity 78.9%; Pred. No. 5.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CAGTCGATCAGTACGAG 20
 DB 3 CTTGCGATCAGTACGAG 21

RESULT 8
 AAAL1514
 AAAL1514 standard; DNA; 27 BP.

XX AAAL1514;
 XX 04-SEP-2000 (first entry)

XX PCR primer for DNA downstream of taaA.
 XX Virulence protein; taaA, tatB, tatC, tatE; mdgQ, creG; recG, yggN;
 XX eckA; iroD; iroC; iroE; md2; msl; vaccine; infection;
 XX Gram negative bacterium; PCR primer; ss.

XX Escherichia coli.
 XX WQ200028038-A2.
 XX 18-MAY-2000.

XX 09-NOV-1999; 99WC-GB03721.
 XX 98GB-0024569.
 XX 09-NOV-1998; 98GB-0024570.
 XX 09-NOV-1998; 98GB-0024571.
 XX 17-DEC-1998; 98GB-0027815.
 XX 17-DEC-1998; 98GB-0027816.
 XX 17-DEC-1998; 98GB-0027818.
 XX 17-DEC-1998; 98GB-0027819.
 XX 13-JAN-1999; 98GB-0000710.
 XX 13-JAN-1999; 98GB-0000711.
 XX 28-JAN-1999; 99GB-0001515.
 XX (MCR-) MICROSCIENCE LTD.

XX Crooke HR, Clarke EB, Everatt PH, Dougan G, Holden DM, Shea JE;
 XX Feldman NG.
 XX WPI; 2000-376550/32.

XX Peptide encoded by an operon including genes from Escherichia coli for
 XX screening potential drugs, detecting virulence and treating conditions
 XX associated with infection by a Gram negative bacterium -
 XX Example 6; Page 10; 122pp; English.

XX PCR primers AAAL1513-94 were used to amplify DNA downstream of taaA.
 XX PCR activities were performed with primers which, when
 XX are encoded by an operon including recA, tatB, tatC, creC,
 XX recG, yggN, eckA, iroD, iroC, iroE, md2 or msl-6 genes obtained from
 XX Escherichia coli X1. The virulence proteins and polynucleotides, and
 XX Escherichia coli X1. The virulence proteins and polynucleotides, and
 XX detection of virulence, and for treating or preventing conditions
 XX associated with infection by a Gram negative bacterium particularly
 XX Escherichia coli.

XX Sequence 27 BP; 8 A; 10 C; 4 G; 5 T; 0 other;
 Query Match 63.0%; Score 12.6; DB 21; Length 27;
 Best Local Similarity 78.9%; Pred. No. 5.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CAGTCGATCAGTACGAG 20
 DB 1 CAGTCGATCAGTACGAG 19

RESULT 9
 AAAL1107
 AAAL1107 standard; DNA; 20 BP.

XX AAAL1107;
 XX 29-NOV-2000 (first entry)

XX Forward PCR primer for loblolly pine locus KIPF65.
 XX PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
 XX microsatellite DNA repeat; genetic marker; mapping; inheritance study;
 XX population genetics study; plant breeding programme; ss.

XX Pinus taeda.
 XX WQ300042210-A2.
 XX 20-JUL-2000.

XX 06-JAN-2000; 2000WO-US00325.
 XX 15-JAN-1999; 99US-0212884.
 XX 15-JAN-1999; 99US-0212785.

XX (INTO) INT PAPER CO.
 XX (ECHT/) ECHT C S O.
 XX (USDA) US SEC OF AGRIC.

XX Echt CS, Nelson CD;
 XX WPI; 2000-482836/42.

XX Polynucleotide having simple sequence repeat useful as markers in
 XX inheritance study of a commercially important trait in a plant breeding
 XX program -

XX Claim 6; Page 23; 57pp; English.

XX The present invention relates to loblolly pine polynucleotides with one
 XX or more simple sequence repeats (SSRs) (see AA0245-A1432). SSRs are
 XX also known as microsatellites. DNA near the SSRs can be used as genetic
 XX markers for genetic mapping, population genetics studies and inheritance
 XX studies in various plant breeding programmes. The present sequence is a
 XX simple sequence repeat (SSR) located in the loblolly pine genome. The
 XX genomic DNA sample.

XX Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 other;
 Query Match 61.0%; Score 12.2; DB 21; Length 20;
 Best Local Similarity 82.4%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TGATCGATCAGTACGAG 20
 DB 1 TGATCGATCAGTACGAG 17

RESULT 10
 AAU43370/C

CC and comprises one of the generic sequences 5'-NNNT-CpG-WNN-3' or
 CC 5'-AT-CpG-R-3'. The CpG-CpG or umethylyated CpG-CpG oligonucleotide
 CC oligonucleotides optionally have phosphothioate linkages which make
 CC them more resistant to degradation. The invention also relates to an
 CC immunogenic composition comprising a cell-mediated response or a humoral
 CC response, and a targeting agent and a pharmaceutical composition
 CC comprising the oligonucleotide delivery complex. The oligonucleotide
 CC are able to induce either a cell-mediated (T-cell) response or a humoral
 CC 5'-AT-CpG-R-3' being able to induce a cell-mediated response, and those
 CC of the sequence 5'-NNNT-CpG-WNN-3' being able to induce a humoral
 CC response. It is thought that after administration, the oligonucleotide
 CC enters the cell, and the immunogenic composition is released from the
 CC killer (NK) cells. A cell-mediated or humoral response can then occur by
 CC the action of the immunogenic composition. The immunogenic composition
 CC is useful for treating, preventing or ameliorating an allergic reaction
 CC (preferably asthma), or an infection, where an immunogenic CpG
 CC oligonucleotide is administered either alone or in combination with an
 CC adjuvant. The immunogenic composition is also useful for treating
 CC conditions which may be treated include eczema, allergic rhinitis, hayfever,
 CC urticaria, food allergies and other atopic conditions, and the
 CC infections which may be treated include viral, bacterial, fungal and
 CC schistosomiasis. Immune response induction may also be used in the
 CC treatment of an autoimmune disorder (e.g., lupus erythematosus,
 CC immune osteoarthritis and multiple sclerosis). The response associated with
 CC immune cell-defining and multiple activating CpG oligonucleotides is an
 CC agent of biological warfare. An immunogenic CpG oligonucleotide, either
 CC alone or in combination with an anti-cancer agent, is useful for treating
 CC cancer. The immunogenic composition is also useful for treating
 CC autoimmune therapy and to improve the efficacy of vaccine. The
 CC oligonucleotide is preferably administered to lymphocytes *ex vivo*,
 CC producing activated lymphocytes which are then administered to the host.
 CC The present invention represents an immunogenic CpG oligonucleotide
 CC of the invention.

Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;

Query Match 65.0%; Score 13; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCATCATGCATCAT 13

13 GCATCATGCATCAT 1

RESULT 6

AAK46523; C
 AAK46523 standard; DNA, 17 BP.

05-JUN-2002 (first entry)
 Immunostimulatory umethylyated CpG oligonucleotide #113.

umethylyated CpG, oligonucleotide, ODN; virucide; vaccine;
 Parainfluenza; P protein; respiratory syncytial virus; RSV;
 Respiratory syncytial virus; RSV; Respiratory syncytial virus;
 bronchopulmonary dysplasia, congenital heart condition, etc.

Synthetic.

MO200211761-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-A1633.

10-AUG-2000; 2000US-22401P.

01-SEP-2001; 2000US-22301P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX Mond JU, Prince G, Kliman DM;
 XX WPI; 2002-227118/28.
 XX Vaccine for immunising patient against respiratory syncytial virus. Has
 XX a nucleotide sequence which is a derivative of the sequence followed by guanine
 XX linked by phosphate bond-oligodeoxynucleotides

XX Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a
 CC Parainfluenza virus, and one or more CpG (cytosine followed by
 CC guanine) dinucleotides. The vaccine is useful for vaccinating a patient
 CC of the Parainfluenza family e.g. respiratory syncytial virus (RSV).
 CC The primary cause of viral bronchiolitis and pneumonia in infants and
 CC children is the Parainfluenza virus. The virus is particularly
 CC particularly implicated in death of infants that are premature, have
 CC bronchopulmonary dysplasia, or congenital heart conditions. This
 CC sequence represents an oligodeoxynucleotide that can be used in the
 CC creation of the vaccine.

XX Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;

Query Match 65.0%; Score 13; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATCATGCATCAT 13

DB 13 GCATCATGCATCAT 1

RESULT 7

AAQ46972
 AAQ46972 standard; DNA, 26 BP.

AC AAQ46972;

25-JUN-1994 (first entry)

Helper Probe #7 to detect Streptococcus pyogenes RNA.

group A beta-haemolytic Streptococcus; S pyogenes; ribosomal RNA;
 respiratory tract infection; sinusitis; pharyngitis; meningitis;
 tonsillitis; septicaemia; pyoderma; endocarditis; impetigo;
 Helper probe, 86.

OS Synthetic.

US522831-A.

03-AUG-1993.

28-JUN-1991; 91US-0720586.

28-JUN-1991; 91US-0720586.

GENPRO-1 GEN PROBE INC.

Hammond PW, Millman CL;

WPI; 1991-257892/32.

New nucleotide polymers used as probes for detection of
 PT related species when used alone or as a mix
 PT related species when used alone or as a mix

XX Claim 7; Column 13; 9pp; English.

Copied from 09980559 on 05/19/2004

GenCore version 5.1.6

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GENCORE VERSION 3.1.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-540-843-B

Perfect score: 20

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8 95/7557 :DANCYRAD

Total number of hits satis:

1. *Journal of the American Medical Association*, 1997; 277: 1033-1038.

Minimum DB seq length: 0
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SUMMARIES

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2	20	100	20	AA54412	Malonacetic acid
3	16	68	29	AZ73951	Immunogenic alpha
4	16	68	29	AZ73951	Immunogenic alpha
5	15	65	0	AZ80678	Immunogenic CpG
6	15	65	0	AZ80678	Immunogenic CpG
7	13	63	27	AAK46523	Immunostimulatory
8	12	63	27	AAK46523	Immunostimulatory
9	12	63	27	AA15454	PCR primer for DNA
10	12	63	27	AA15454	PCR primer for DNA

9	12.2	61.0	20	21	AAAT74107	Forward PCR primer
C 10	12.2	61.0	20	21	AAAT45370	Human MBL cDNA and
C 11	12.2	61.0	21	22	AAAT45370	Human mut L homolog
C 12	12.2	61.0	21	22	AAAT45370	Oct-dpase probe use
C 13	12.2	61.0	21	22	AAAT45370	S. pneumoniae pbpl
C 14	12.2	61.0	23	22	AAH02033	Human zinc finger
C 15	12.2	61.0	24	24	AAH14112	Oligonucleotide ad
C 16	12.2	61.0	24	24	AAH07960	Oligonucleotide ad
C 17	12.2	61.0	24	24	AAH08001	Oligonucleotide ad
C 18	12.2	61.0	24	24	AAH08001	Oligonucleotide ad
C 19	12.2	61.0	24	24	AAH08001	Oligonucleotide ad
C 20	12.2	61.0	12	21	AAAT2016	Oligonucleotide ad
C 21	12.2	61.0	12	21	AAAT2016	Oligonucleotide ad
C 22	12.2	61.0	22	22	AAH22273	Oligonucleotide ad
C 23	12.2	61.0	22	22	AAH22273	Oligonucleotide ad
C 24	12.2	61.0	24	24	AAH18044	Oligonucleotide ad
C 25	12.2	61.0	24	24	AAH18044	Oligonucleotide ad
C 26	12.2	61.0	24	24	AAH18044	Oligonucleotide ad
C 27	12.2	61.0	24	24	AAH18044	Oligonucleotide ad
C 28	12.2	61.0	24	24	AAH18044	Oligonucleotide ad
C 29	11.8	59.0	17	20	AAV3571	Human B-raf subter
C 30	11.8	59.0	18	21	AAV3571	Human B-raf subter
C 31	11.8	59.0	18	21	AAV3571	Human B-raf subter
C 32	11.8	59.0	20	24	AAH4436	Green filamentous
C 33	11.8	59.0	22	22	AAH1139	S. pneumoniae pbpl
C 34	11.8	59.0	22	22	AAH1139	S. pneumoniae pbpl
C 35	11.8	59.0	22	22	AAH1139	S. pneumoniae pbpl
C 36	11.8	59.0	22	22	AAH1139	S. pneumoniae pbpl
C 37	11.8	59.0	26	24	AAH6093	Yeast cytochrome
C 38	11.8	59.0	29	24	AAH6093	Yeast cytochrome
C 39	11.8	59.0	30	25	AAH4436	Yeast cytochrome
C 40	11.8	59.0	30	25	AAH4436	Yeast cytochrome
C 41	11.8	59.0	30	25	AAH4436	Yeast cytochrome
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C 44	11.8	59.0	30	25	AAH4436	Yeast cytochrome
C 45	11.6	58.0	18	22	AAH22519	PCR primer used to
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C 50	11.6	58.0	18	22	AAH22519	PCR primer used to


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1 (bases 1 to 15)
REFERENCE Choudhary, G., Hahnenberger, K., Kueskes, P.J., Lichtenwalter, K. and
AUTHORS Hancock, M.S.
TITLE Methods for identifying a plurality of chemicals on a substrate by
electrophoretic self-assembly
JOURNAL Patent: US 6107038-A 1 22-AUG-2000;
FEATURES Location/Qualifiers
source
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13 GONTATCATCAT 2
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RESULT 15
ACCESSION AX133943
DEFINITION 15 bp DNA linear PAT 15-MAY-2001
SEQUENCE 2 from Patent WO0127327.
ACCESSION AX133943
DESCRIPTION AX133943.1 GI:14139884
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini, Hominoidea; Homo.
REFERENCE Brennan, T.M., Chatelein, F. and Berninger, M.
AUTHORS Brennan, T.M., Chatelein, F. and Berninger, M.
TITLE Methods and apparatus for performing large numbers of reactions
JOURNAL Patent: WO 0127327-A 2 19-APR-2001;
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KEYWORDS
SOURCE
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Db 3 CAGGATCATCTAGCA 19

RESULT 10
LOCUS AR445579/c 24 bp DNA linear PAT 03-JUL-2002
DEFINITION AR445579 2034 from Patent WO011664.
ACCESSION AR445579.1 GI:21692860
VERSION AR445579.1 GI:21692860
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VERSION
KEYWORDS
SOURCE
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Qy 1 GCGTCATCTAGCACT 17
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RESULT 11
LOCUS AR203427 30 bp DNA linear PAT 20-JUN-2002
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ACCESSION AR203427.1 GI:21499813
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RESULT 12
LOCUS AR216687 43 from patent US 645324. linear PAT 20-DEC-2002
DEFINITION AR216687
ACCESSION AR216687.1 GI:27280788
VERSION AR216687.1 GI:27280788
KEYWORDS
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AUTHORS
TITLE
JOURNAL
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RESULT 13
LOCUS AR106386 15 bp DNA linear PAT 14-FEB-2001
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ACCESSION AR106386.1 GI:12820916
VERSION AR106386.1 GI:12820916
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AUTHORS
TITLE
JOURNAL
FEATURES
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VERSION
KEYWORDS
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RESULT 14
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DEFINITION AR106386
ACCESSION AR106386.1 GI:12820916
VERSION AR106386.1 GI:12820916
KEYWORDS
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TITLE
JOURNAL
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ORIGIN

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VERSION
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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ACCESSION
VERSION
KEYWORDS
SOURCE
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LOCUS      6 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 21 from patent US 6416994.
ACCESSION AR217681
VERSION AR217681.1 GI:23317552
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
Unclassified
Haseltine, W.A., Ruben, S.M., Wei, Y.-F., Adams, M.D.,
Kirkness, E.F., Frazer, C.M., Fuldner, R.A., Kirkness, E.F. and
Rosen, C.A.
Human DNA mismatch repair proteins
Patent: US 6416994-A 21 09-JUN-2002;
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LOCUS      8 bp DNA linear PAT 20-DEC-2002
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ACCESSION AR255705
VERSION AR255705.1 GI:27304802
KEYWORDS
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ORGANISM
REFERENCE
1 (bases 1 to 21)
Unclassified
Adams, M.D., Fleischmann, R.D., Frazer, C.M., Fuldner, R.A.,
Kirkness, E.F., Haseltine, W.A., Rosen, C.A., Ruben, S. and Wei, Y.-F.
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Db 18 ATGCATCATCTGTCAC 2
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LOCUS      9 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 2036 from Patent WO012660.
ACCESSION AX11293
VERSION AX11293.1 GI:13927585
KEYWORDS
SOURCE
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REFERENCE
1 (bases 1 to 20)
Unclassified
Bergerson, M.G., Bolesinot, M., Huletsky, A., m Nard, C., Quellet, M.,
Picaud, P.J. and Roy, P.H.
Highly conserved genes and their use to generate probes and primers
for the detection of infectious agents
Patent: WO 012660-A 2026 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
LOCUS/Qualifiers
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 2 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 3 TITLE OF INVENTION: Hepatitis C Virus Infection
 4 CURRENT APPLICATION NUMBER: US/09/817,879
 5 CURRENT FILING DATE: 2001-03-26
 6 NUMBER OF SEQ ID NOS: 9703
 7 SOFTWARE: EntSeq for Windows version 3.0
 8 SEQ ID NO 424
 9 LENGTH: 13

10 TYPE: RNA
 11 FEATURE: Artificial Sequence
 12 NAME/KEY: misc_feature
 13 LOCATION: INFORMATION: oligonucleotide substrate
 14 COORDINATES: 1-13
 15 US-09-817-879-4624

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1 ACTATGA 7
 2 TTTT 11
 3 AGAAGCA 12

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 28-09-875-440-22/C
 Sequence 22, Application US/09875440
 GENERAL INFORMATION:
 APPLICANT: Reinhard, Christoph
 APPLICANT: Jefferson, Anne B.
 APPLICANT: Reinhard, Christoph
 APPLICANT: Randazzo, Filippo
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
 FILING DATE: 2001-06-05
 CURRENT APPLICATION NUMBER: US/09/875,440
 CURRENT FILING DATE: 2001-06-05
 SOFTWARE: EntSeq for Windows version 4.0
 SEQ ID NO 22
 LENGTH: 14

10 ORGANISM: Artificial Sequence
 11 FEATURE:
 12 OTHER INFORMATION: Oligonucleotide NET-4 oligo 968 used for in-situ
 13 INFORMATION: Hybridization
 14 US-09-875-440-22

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 Job time : 82.6076 secs

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QY      1 AGTATGA 7
DB      10 AGTATGA 4

RESULT 10
US-10-033-145-1423/c Location US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENETIC CORPORATION
; APPLICANT: KOCCH, TROELS
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1423
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone
US-10-033-145-1423
Query Match 100.0% Score 7; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTATGA 7
DB      7 AGTATGA 1

RESULT 11
US-10-033-145-1423/c Location US/10150779A
; Publication No. US20030125241A1
; GENERAL INFORMATION:
; APPLICANT: KOCCH, TROELS
; APPLICANT: KOCCH, TROELS
; APPLICANT: ORUM, HENRICK
; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
; CURRENT FILING DATE: 2003-02-07
; FILE REFERENCE: 55704 (45120)
; NUMBER OF SEQ ID NOS: 16
; PRIOR APPLICATION NUMBER: 60/291,830
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/291,830
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone
US-10-150-779A-15
Query Match 100.0% Score 7; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTATGA 7
DB      11 AGTATGA 5

```

```

RESULT 12
US-10-150-779A-16/c
; Sequence 16, Application US/10150779A
; Publication No. US20030125241A1
; GENERAL INFORMATION:
; APPLICANT: KOCCH, TROELS
; APPLICANT: KOCCH, TROELS
; APPLICANT: ORUM, HENRICK
; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
; CURRENT FILING DATE: 2003-02-07
; FILE REFERENCE: 55704 (45120)
; NUMBER OF SEQ ID NOS: 16
; PRIOR APPLICATION NUMBER: 60/291,830
; CURRENT FILING DATE: 2003-02-07
; FILE REFERENCE: 55704 (45120)
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone
US-10-150-779A-16
Query Match 100.0% Score 7; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTATGA 7
DB      11 AGTATGA 5

RESULT 13
US-09-740-332-4624
; Sequence 15, Application US/09740332
; Publication No. US20030125279A1
; GENERAL INFORMATION:
; APPLICANT: Ribosyme Pharmaceuticals Inc.
; APPLICANT: Ribosyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003 US/09/740,332
; CURRENT FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: Patent in version 3.0
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: DNA oligonucleotide substrate
US-09-740-332-4624
Query Match 100.0% Score 7; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGTATGA 7
DB      6 AGTATGA 12

RESULT 14
US-09-817-879-4624
; Sequence 4624, Application US/09817879
; Publication No. US2003017131A1
; GENERAL INFORMATION:

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1

Query Match      100.0%; Score 7; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATCA 7
    |||||
Db 2 AGTATCA 8

RESULT 6
Sequence 1, Application US/1012263
Publication No. US2003032611A1
GENERAL INFORMATION:
APPLICANT: ELLER, Barbara A.
APPLICANT: ELLER, Mark S.
APPLICANT: YEAT, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
FILE REFERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US/10122-633
PRIOR APPLICATION NUMBER: US 09/540-843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1

Query Match      100.0%; Score 7; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATCA 7
    |||||
Db 2 AGTATCA 8

RESULT 7
Sequence 31, Application US/09398399
Publication No. US2003032611A1
GENERAL INFORMATION:
APPLICANT: DELENSTARR, GLENDA C.
APPLICANT: DELENSTARR, KEVIN M.
APPLICANT: LEBER, LESLIE B.
APPLICANT: OVERMAN, LESLIE B.
APPLICANT: SMYRNAS, NICHOLAS M.
APPLICANT: MOJER, PAUL K.
TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING OF NUCLEIC
ACIDS TO SURFACES
CURRENT APPLICATION NUMBER: US/09/398,399
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Ver. 2.0
SEQ ID NO 31
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-398-399-31

Query Match      100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATCA 7
    |||||
Db 1 AGTATCA 7

RESULT 8
Sequence 3, Application US/09893931
Publication No. US20030068292A1
GENERAL INFORMATION:
APPLICANT: DELENSTARR, Glend C.
APPLICANT: DELENSTARR, Mark S.
APPLICANT: SANF, Theodore R.
TITLE OF INVENTION: Arrays Having Background Features and
Methods for Using the Same
CURRENT APPLICATION NUMBER: US/09/899,381
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: US 09/398,399
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic probe
US-09-899-381-31

Query Match      100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATCA 7
    |||||
Db 1 AGTATCA 7

RESULT 9
Sequence 3, Application US/10329465
Publication No. US20030165949A1
GENERAL INFORMATION:
APPLICANT: Wang et al.
TITLE OF INVENTION: FUSION
FILE REFERENCE: 27373/37528A
CURRENT APPLICATION NUMBER: US/10/329,465
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: US 60/343,426
PRIOR FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq Version 3.1
SEQ ID NO 30
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial sequence
OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-30

Query Match      100.0%; Score 7; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

Db          1  AATATGA 7

RESULT 2
US-10-122-630-7
; Sequence 2, Application US/1012630
; Publication No. US2003032610A1
; ORGANISM: Homo sapiens
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPE: DNA
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7

Query Match      100.0% Score 7; DB 15; Length 7;
Beet Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1  AATATGA 7

RESULT 3
US-10-122-633-3
; Sequence 3, Application US/1012633
; Publication No. US2003032610A1
; ORGANISM: Homo sapiens
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 7
TYPE: DNA
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match      100.0% Score 7; DB 15; Length 7;
Beet Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1  AATATGA 7

RESULT 4
US-10-122-633-7
; Sequence 4, Application US/1012633
; Publication No. US2003032610A1
; ORGANISM: Homo sapiens
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPE: DNA
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7

Query Match      100.0% Score 7; DB 15; Length 7;
Beet Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1  AATATGA 7

RESULT 5
US-10-122-630-1
; Sequence 1, Application US/1012630
; Publication No. US2003032610A1
; ORGANISM: Homo sapiens
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/00386
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 9
TYPE: DNA
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

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GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00, Search time 81.6976 Seconds
296.896 Million cell updates/sec

Title: US-09-540-843-7

Parallels: 1 agents 7

Sequence: 1

Scoring table: IDENTITY.MUC

Gapop 10.0, Gapext 1.0

Searched: 2263442 seqs, 1730637950 residues

Procal number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 9

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 15 summaries

Database:

Published Applications NA.:

- 1: /csm2_6/pdata1/pubna/usgr_pucomb.seq.
- 2: /csm2_6/pdata1/pubna/usgr_pucomb.seq.
- 3: /csm2_6/pdata1/pubna/usg2_new_pu.seq.
- 4: /csm2_6/pdata1/pubna/usg2_new_pu.seq.
- 5: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 6: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 7: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 8: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 9: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 10: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 11: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 12: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 13: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 14: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 15: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 16: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 17: /csm2_6/pdata1/pubna/usg2_pucomb.seq.
- 18: /csm2_6/pdata1/pubna/usg2_pucomb.seq.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	15	Sequence 3, Appl
2	7	100.0	7	15	Sequence 3, Appl
3	7	100.0	7	15	Sequence 3, Appl
4	7	100.0	7	15	Sequence 3, Appl
5	7	100.0	9	15	Sequence 3, Appl
6	7	100.0	9	15	Sequence 3, Appl
7	100.0	9	15	US-10-122-630-1	Sequence 3, Appl
8	7	100.0	10	9	Sequence 3, Appl
9	7	100.0	10	9	Sequence 3, Appl
10	7	100.0	10	13	Sequence 30, Appl
11	7	100.0	10	13	Sequence 30, Appl
12	7	100.0	12	15	Sequence 15, Appl
13	7	100.0	13	11	Sequence 16, Appl
14	7	100.0	13	11	Sequence 16, Appl
15	7	100.0	14	10	Sequence 1624, Ap
16	7	100.0	14	10	Sequence 1624, Ap
17	7	100.0	14	10	Sequence 1624, Ap
18	7	100.0	14	10	Sequence 1624, Ap
19	7	100.0	14	10	Sequence 1624, Ap
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23	7	100.0	14	10	Sequence 1624, Ap
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26	7	100.0	14	10	Sequence 1624, Ap
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100	7	100.0	14	10	Sequence 1624, Ap

16	7	100.0	15	9	US-09-504-311A-527
17	7	100.0	15	9	US-09-504-311A-527
18	7	100.0	15	9	US-09-504-311A-529
19	7	100.0	15	9	US-09-504-311A-527
20	7	100.0	15	9	US-09-504-311A-527
21	7	100.0	15	9	US-09-504-311A-527
22	7	100.0	15	9	US-09-398-350-30
23	7	100.0	15	9	US-09-999-181-30
24	7	100.0	15	9	US-09-999-181-30
25	7	100.0	15	9	US-09-274-553D-528
26	7	100.0	15	9	US-09-274-553D-528
27	7	100.0	15	9	US-09-274-553D-528
28	7	100.0	15	9	US-09-274-553D-528
29	7	100.0	15	9	US-09-274-553D-528
30	7	100.0	15	10	US-09-274-553D-528
31	7	100.0	15	10	US-09-274-553D-528
32	7	100.0	15	10	US-09-274-553D-528
33	7	100.0	15	11	US-09-740-332-4571
34	7	100.0	15	11	US-09-817-879-4558
35	7	100.0	15	11	US-09-817-879-4558
36	7	100.0	15	13	US-10-400-850-8871
37	7	100.0	15	13	US-10-400-850-8871
38	7	100.0	15	13	US-10-400-850-8871
39	7	100.0	17	9	US-09-866-108-2749
40	7	100.0	17	9	US-09-866-108-2749
41	7	100.0	17	9	US-09-866-108-2752
42	7	100.0	17	9	US-09-866-108-2752
43	7	100.0	17	9	US-09-866-108-2752
44	7	100.0	17	9	US-09-866-108-2755
45	7	100.0	17	9	US-09-866-108-2755

ALIGNMENTS

RESULT 1
US-10-122-630-3
Sequence 3, Application US/10122630
GENERAL INFORMATION
APPLICANT: Gluchrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
REFERENCE: 00541888-018/16/1122_630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/467,012
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
TYPE: DNA
ORGANISM: Artificial Sequence
COMMENT: Synthetic DNA Fragment
US-10-122-630-3

Query Match 100.0%, Score 7, DB 15, Length 7,
Best Local Similarity 100.0%, Pos No. 4, Neg. 0,
Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
1 ACTATGCA 7

STRANDS: single
TOPOLOGY: linear

US-08-485-133-28

100.0%; Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

DB 9 AGTATGA 15

RESULT 14
US-09-094-714A-33/C Location US/09094714A
Parent No. 6117847

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nicholas M. Dean
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 8.0

COMPUTER APPLICATION DATA:

APPLICATION NUMBER: US/09/094,714A

FILING DATE: June 15, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,269

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/478,178

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/089,996

FILING DATE: 09-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/852,852

FILING DATE: 16-MAR-1992

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO. 33:

LENGTH: 15

TYPE: nucleic acid

SEQUENCE CHARACTERISTICS:

STRANDS: single

TOPOLOGY: linear

US-09-094-714A-33

Query Match

Best Local Similarity 100.0%; Score 7; DB 3; Length 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

DB 12 AGTATGA 6

RESULT 15

US-09-094-714A-34/C

Sequence 34; Application US/09094714A

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nicholas M. Dean

TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 8.0

COMPUTER APPLICATION DATA:

APPLICATION NUMBER: US/09/094,714A

FILING DATE: June 15, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,269

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/478,178

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/089,996

FILING DATE: 09-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/852,852

FILING DATE: 16-MAR-1992

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO. 34:

LENGTH: 15

TYPE: nucleic acid

SEQUENCE CHARACTERISTICS:

STRANDS: single

TOPOLOGY: linear

US-09-094-714A-34

Query Match

Best Local Similarity 100.0%; Score 7; DB 3; Length 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

DB 14 AGTATGA 8

Search completed: January 1, 2004, 00:32:19

Job time : 28.3136 secs

NINGER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 151 West Fifth Street
 CITY: Sulte 700
 STATE: California
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSO Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER US/08/585-6848
 FILING DATE: January 16, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 67/000-951
 FILING DATE: July 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,127
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 130:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 STRANDNESS: single
 TOPOLOGY: linear
 US-08-585-6848-130
 Query Match 100.0%; Score 7; DB 2; Length 15;
 Best Local Similarity 71.4%; pred. No. 0.6e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 INFORMATION FOR SEQ ID NO: 130:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 STRANDNESS: single
 TOPOLOGY: linear
 US-08-585-6848-130
 Query Match 100.0%; Score 7; DB 2; Length 15;
 Best Local Similarity 71.4%; pred. No. 0.6e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 INFORMATION FOR SEQ ID NO: 130:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 STRANDNESS: single
 TOPOLOGY: linear
 US-08-585-6848-130

NINGER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 151 West Fifth Street
 CITY: Sulte 700
 STATE: California
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSO Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER US/08/585-6848
 FILING DATE: January 16, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 67/000-951
 FILING DATE: July 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,127
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 131:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 STRANDNESS: single
 TOPOLOGY: linear
 US-08-585-6848-131
 Query Match 100.0%; Score 7; DB 2; Length 15;
 Best Local Similarity 71.4%; pred. No. 0.6e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 INFORMATION FOR SEQ ID NO: 131:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 STRANDNESS: single
 TOPOLOGY: linear
 US-08-585-6848-131

TELEPHONE: (213) 485-1600
FAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 327:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 base pairs
TYPE: nucleic acid
STRANDNESS: single
US-08-334-847-327

Query Match 100.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
5 AGAUGA 11

RESULT 9
Sequence 9, Application US/08671071B
GENERAL INFORMATION:
APPLICANT: Grandgenett, Duane
TITLE OF INVENTION: An in vitro method for concerted integration of
sequences of tumor DNA molecules using retroviral integrase proteins.
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA: 08/671,071B
FILING DATE: 06/27/96
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 577-8406
TELEFAX: (314) 577-8406
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: double
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Combination of avian or HIV-1 retrovirus
ORIGINAL SOURCE: DNA, p197 plasmid and p08M plasmid.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

Query Match 100.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
9 AGAUGA 3

RESULT 10
Sequence 10, Application US/08747121
GENERAL INFORMATION:
APPLICANT: Grandgenett, Duane
TITLE OF INVENTION: An in vitro method for concerted integration of
sequences of tumor DNA molecules using retroviral integrase proteins.
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA: 08/747,121
FILING DATE: 08-Nov-1996
CLASSIFICATION: 514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 186-9864
TELEFAX: (212) 186-9864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Same as in 2.v1.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

Query Match 100.0%; Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
15 AGATGCA 9

RESULT 11
Sequence 11, Application US/08585648
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA: 08/585,648
FILING DATE: 08-Nov-1996
CLASSIFICATION: 514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 186-9864
TELEFAX: (212) 186-9864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Same as in 2.v1.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

Query Match 100.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
9 AGAUGA 3

RESULT 12
Sequence 12, Application US/08585648
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA: 08/585,648
FILING DATE: 08-Nov-1996
CLASSIFICATION: 514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 186-9864
TELEFAX: (212) 186-9864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Same as in 2.v1.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

TELEPHONE: (213) 485-1600
FAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 327:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 base pairs
TYPE: nucleic acid
STRANDNESS: single
US-08-334-847-327

Query Match 100.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
5 AGAUGA 11

RESULT 9
Sequence 9, Application US/08671071B
GENERAL INFORMATION:
APPLICANT: Grandgenett, Duane
TITLE OF INVENTION: An in vitro method for concerted integration of
sequences of tumor DNA molecules using retroviral integrase proteins.
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA: 08/671,071
FILING DATE: 06/27/96
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 577-8406
TELEFAX: (314) 577-8406
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: double
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Combination of avian or HIV-1 retrovirus
ORIGINAL SOURCE: DNA, p197 plasmid and p08M plasmid.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

Query Match 100.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
9 AGAUGA 3

RESULT 10
Sequence 10, Application US/08747121
GENERAL INFORMATION:
APPLICANT: Grandgenett, Duane
TITLE OF INVENTION: An in vitro method for concerted integration of
sequences of tumor DNA molecules using retroviral integrase proteins.
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA: 08/747,121
FILING DATE: 08-Nov-1996
CLASSIFICATION: 514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 186-9864
TELEFAX: (212) 186-9864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Same as in 2.v1.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

Query Match 100.0%; Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
15 AGATGCA 9

RESULT 11
Sequence 11, Application US/08585648
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA: 08/585,648
FILING DATE: 08-Nov-1996
CLASSIFICATION: 514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 186-9864
TELEFAX: (212) 186-9864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Same as in 2.v1.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

Query Match 100.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No. 8.66+03; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGATGCA 7
9 AGAUGA 3

RESULT 12
Sequence 12, Application US/08585648
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA: 08/585,648
FILING DATE: 08-Nov-1996
CLASSIFICATION: 514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 186-9864
TELEFAX: (212) 186-9864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: Same as in 2.v1.
IMMEDIATE SOURCE: Same as in 2.v1.
FEATURES:
OTHER INFORMATION: The sequence is the bottom strand of
the p197 plasmid.
OTHER INFORMATION: Figure 14 of the original application.

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1  TITLE OF INVENTION:  AND METHODS OF USE THEREOF
2  NUMBER OF SEQUENCES:  14
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Dennis & Edmonds
5  ADDRESS:  115 Avenue of the Americas
6  CITY:  New York
7  STATE:  NY
8  COUNTRY:  USA
9  PUBLICATION NUMBER:  711
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Diskette
12 OPERATING SYSTEM:  IBM Compatible
13 SOFTWARE:  FastSeq Version 2.0
14 CURRENT APPLICATION DATA:
15 FILING DATE:  08-NOV-1998
16 FILING DATE:  08-NOV-1998
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER:
19 FILING DATE:
20 ATTORNEY/AGENT INFORMATION:
21 NAME:  Newman, Geraldine J.
22 REGISTRATION NUMBER:  8511-009
23 REFERENCE/DOCKET NUMBER:  8511-009
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE:  (212) 699-0990
26 TELEFAX:  (212) 699-0990
27 TELETYPE:  66141 PENNIE
28 INFORMATION FOR SEQ ID NO:  4:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH:  14 base pairs
31 TYPE:  nucleic acid
32 STRANDNESS:  single
33 FEATURE:
34 NAME/KEY:  Modified Base
35 LOCATION:  1
36 ORGANISM:  Homo sapiens
37 DB-08-744-905A-4
38 Query Match 100.0%, Score 7, DB 2; Length 14;
39 Query Locs Similarity 1.0101, 8.0e-03;
40 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1  MEDIUM TYPE:  storage
2  COMPUTER:  IBM Compatible
3  OPERATING SYSTEM:  IBM P.C. DOS 5.0
4  SOFTWARE:  Word Perfect 5.1
5  CURRENT APPLICATION DATA:
6  FILING DATE:  08-NOV-1998
7  APPLICATION NUMBER:  US/08/334.847
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER:
10 FILING DATE:
11 ATTORNEY/AGENT INFORMATION:
12 NAME:  Mathurs, Richard J.
13 REGISTRATION NUMBER:  327
14 REFERENCE/DOCKET NUMBER:  209/032
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE:  (212) 353-4895-1600
17 TELEFAX:  (212) 353-0446
18 TELETYPE:  67-3510
19 INFORMATION FOR SEQ ID NO:  24:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH:  15 base pairs
22 TYPE:  nucleic acid
23 STRANDNESS:  single
24 FEATURE:
25 NAME/KEY:  Modified Base
26 LOCATION:  1
27 ORGANISM:  Homo sapiens
28 DB-08-334-847-24
29 Query Match 100.0%, Score 7, DB 1; Length 15;
30 Query Locs Similarity 1.0101, 8.0e-03;
31 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ EARLIER FILING DATE: 1995-06-06
/ SOFTWARE: PatSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 9
/ ORGANISM: Artificial Sequence
/ FEATURE: INFORMATION: DNA Fragment
US-09-048-927-1

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
2 AGTATGA 8

RESULT 5
Sequence 27, Application US/08485113
GENERAL INFORMATION:
APPLICANT: Goss, Philippe A.
APPLICANT: Mach, Philippe P.
APPLICANT: Michard, Bernard F.
APPLICANT: Michard, Bernard F.
TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING
TITLE OF INVENTION: TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES
INVENTOR: Goss, Philippe A.
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P. O. Box 19928
CITY: Alexandria
STATE: VIRGINIA
ZIP: 22320
COMPUTER READABLE FORM:
APPLICANT: Goss, Philippe A.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT FILING DATE: 2001-08-03
APPLICATION NUMBER: US/08/485.133
FILING DATE: 7-JUN-1995
CLASSIFICATION:
PRELIMINARY CLASSIFICATION: US 08/030.143
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-436-6400
TELEFAX: 703-436-2907
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: Synthetic acid
STANDARDS: None
TOPOLOGY: linear
US-08-485-133-27

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
2 AGTATGA 14

RESULT 6
US-08-744-909A-4/c
Sequence 22, Application US/08744905A
GENERAL INFORMATION:
APPLICANT: Goss, Philippe A.
APPLICANT: Michard, Bernard F.
APPLICANT: Michard, Bernard F.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID
TITLE OF INVENTION: SEQUENCES OF C1-2, A TUMOR SUPPRESSOR GENE,

```

GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05, Search time 27.2025 Seconds
111,581 Million cell updates/sec

Title: US-09-540-843-7
Sequence: 1 agatga 7
Scoring table: IDENTITY NUC
Gapop 10.0, capext 1.0

Searched: 569978 seqe, 220691566 residues
Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 30
Minimum DB seq length: 30
Post-processing: Minimum Match 0%
Maximum E-Value 100%
Listing listed 10 summaries

Database: Issued Patents NA.*

- 1: /cm2_6/prodata//ina/58 COMB seq.*
- 2: /cm2_6/prodata//ina/58 COMB seq.*
- 3: /cm2_6/prodata//ina/68 COMB seq.*
- 4: /cm2_6/prodata//ina/68 COMB seq.*
- 5: /cm2_6/prodata//ina/68 COMB seq.*
- 6: /cm2_6/prodata//ina/68 COMB seq.*

Fred. No. is the number of results predicted by chance to have a
minimum DB seq length of 30 and a maximum E-value of 100% being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Seq. No.	Score	Match	Length	DB ID	Description
1	7	100.0	7	100.0	3	US-09-048-927-3
2	7	100.0	9	3	US-09-048-927-1	Sequence 1, Appl
3	7	100.0	13	4	US-09-222-445-12	Sequence 12, Appl
4	7	100.0	14	2	US-08-485-133-27	Sequence 27, Appl
5	7	100.0	14	2	US-08-485-133-27	Sequence 27, Appl
6	7	100.0	14	2	US-08-744-905A-4	Sequence 4, Appl
7	7	100.0	15	1	US-08-334-447-24	Sequence 24, Appl
8	7	100.0	15	1	US-08-334-447-24	Sequence 24, Appl
9	7	100.0	15	1	US-08-671-071B-2	Sequence 2, Appl
10	7	100.0	15	1	US-08-747-121-4	Sequence 4, Appl
11	7	100.0	15	2	US-08-585-664B-130	Sequence 130, Appl
12	7	100.0	15	2	US-08-585-664B-130	Sequence 130, Appl
13	7	100.0	15	2	US-08-485-133-28	Sequence 28, Appl
14	7	100.0	15	3	US-09-094-714A-33	Sequence 33, Appl
15	7	100.0	15	3	US-09-094-714A-33	Sequence 33, Appl
16	7	100.0	15	3	US-09-094-714A-34	Sequence 34, Appl
17	7	100.0	15	3	US-09-048-927-3	Sequence 3, Appl
18	7	100.0	15	3	US-09-048-927-3	Sequence 3, Appl
19	7	100.0	15	3	US-09-038-972-130	Sequence 130, Appl
20	7	100.0	15	4	US-08-932-146C-7	Sequence 7, Appl
21	7	100.0	15	4	US-08-932-146C-7	Sequence 7, Appl
22	7	100.0	15	4	US-09-253-377-2	Sequence 2, Appl
23	7	100.0	15	4	US-09-253-377-2	Sequence 2, Appl
24	7	100.0	16	1	US-08-719-593-24	Sequence 24, Appl
25	7	100.0	16	2	US-08-256-426B-59	Sequence 59, Appl
26	7	100.0	16	3	US-08-458-814-1	Sequence 1, Appl
27	7	100.0	17	1	US-08-330-93A-461	Sequence 461, Appl

Sequence 461, Appl
Sequence 461, Appl
Sequence 367, Appl
Sequence 367, Appl
Sequence 369, Appl
Sequence 369, Appl
Sequence 811, Appl
Sequence 811, Appl
Sequence 815, Appl
Sequence 815, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 443, Appl
Sequence 443, Appl
Sequence 443, Appl
Sequence 443, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 8, Appl
Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-048-927-3
Sequence 3, Application US/09048927
Patent No. 6147056
APPLICANT: GlaxoSmithKline, Inc.
APPLICANT: GlaxoSmithKline, Inc.
APPLICANT: Year: Mina
APPLICANT: Year: Mina
FILE REFERENCE: B094-68A2
FILE REFERENCE: B094-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT APPLICATION NUMBER: US/09/048,927
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER APPLICATION NUMBER: 08/467,012
NUMBER OF SEQ ID NOS: 295-06-06
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: DNA Fragment
OTHER INFORMATION: DNA Fragment

Query Match
Best Local Similarity 100.0% Score 7, DB 3, Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATGATGA 7
Db 1 AATGATGA 7

RESULT 2
US-09-048-927-1
Sequence 1, Application US/09048927
Patent No. 6147056
APPLICANT: GlaxoSmithKline, Inc.
APPLICANT: GlaxoSmithKline, Inc.
APPLICANT: Year: Mina
APPLICANT: Year: Mina
FILE REFERENCE: B094-68A2
FILE REFERENCE: B094-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT APPLICATION NUMBER: US/09/048,927
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER APPLICATION NUMBER: 08/467,012

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt and resealed with T4 DNA polymerase and T4 ligase. The blunt ends were phosphorylated with T4 polynucleotide kinase. Adaptor oligonucleotides were phosphorylated with T4 polynucleotide kinase. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The selected DNA was prepared from a derivative of pGEM1000 vector (pGEM1000-1) by PCR using primers that flank the HindIII site. The vector was ligated with adaptor complementary to the insert adaptor and ligated into the HindIII site. The ligated DNA was annealed to the adaptor complementary to the insert adaptor and selected for *amp^r* resistance. Chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for *amp^r* resistance.

5 a 6 c 5 g 9 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score: 7; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 AGTATGA 7
Db 22 ACTATGA 16

RESULT 12
LOCUS 25 bp DNA linear GSS 13-JUN-2002

DEFINITION Arabidopsis thaliana genomic clone SALK_075689.48.55.X; genomic

ACCESSION BM52860.1 GI:21423731

VERSION 1.0

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

REFERENCE 1; eukaryotes II; Brassicales; Brassicaceae; Arabidopsis.

A Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,K., Gadrinab

Zimmerman,J. and Ecker,J.R.

Journal of Molecular Biology

Volume 331, Number 1, 1-25, 2002

Abstract

Background

Results

Conclusions

Keywords

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Comments

Copied from 09980559 on 05/19/2004


```

Email: dhunaggenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0086 Row: E Column: 01
Seq primer: CACACGAGAACGACCTATGACC
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/ad_sref="taxon:10090"
/sex="Male"
/ab_ihost="E. coli strain XL10-Gold, TI-resistant, F-"/
/clonetype="Mouse 10kb plasmid UUCGM library"
/musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt ended with T4 DNA polymerase and 5'
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gels
of pMD22 (G114732114) (pA129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert and ligated
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA and transformed into
chemically competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.
6 a 1 c 6 t
BASE COUNT
5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
ORIGIN
Query Match 100.0%; Score 7; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGTATCA 7
10 AGTATCA 16
RESULT 2
2609866 18 bp DNA linear GSS 27-APR-2001
26027414R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM027414 R, genomic survey sequence.
ACCESSION Z5990856
KEYWORDS GSS: Z5990856.1 GI:13622083
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
MAMMALIA; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
REFERENCES Dum.D., Ayoubi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Jain, M., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Seilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weis, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah
Genomic Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84142, USA
Tel: 801.595.5606

Email: dhunaggenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0086 Row: E Column: 01
Seq primer: CACACGAGAACGACCTATGACC
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/ad_sref="taxon:10090"
/sex="Male"
/ab_ihost="E. coli strain XL10-Gold, TI-resistant, F-"/
/clonetype="Mouse 10kb plasmid UUCGM library"
/musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt ended with T4 DNA polymerase and 5'
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gels
of pMD22 (G114732114) (pA129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert and ligated
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA and transformed into
chemically competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.
6 a 1 c 6 t
BASE COUNT
5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95
ORIGIN
Query Match 100.0%; Score 7; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGTATCA 7
10 AGTATCA 16
RESULT 3
2623945 22 bp DNA linear GSS 13-DEC-2000
1M0462010F Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM0462010 F, genomic survey sequence.
ACCESSION Z523945
KEYWORDS GSS: Z523945.1 GI:11746135
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
MAMMALIA; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
REFERENCES Dum.D., Ayoubi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Jain, M., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Seilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah
Genomic Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84142, USA
Tel: 801.595.5606

```

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09, Search time 804.291 Seconds
 211,530 Million cell updates/sec

File: US-09-540-843-7

Sequence: 1 agataga 7

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: en:enba.*

2: en:enba.*

3: en:enba.*

4: en:enba.*

5: en:enba.*

6: en:enba.*

7: en:enba.*

8: en:enba.*

9: en:enba.*

10: en:enba.*

11: en:enba.*

12: en:enba.*

13: en:enba.*

14: en:enba.*

15: en:enba.*

16: en:enba.*

17: en:enba.*

18: en:enba.*

19: en:enba.*

20: en:enba.*

21: en:enba.*

22: en:enba.*

23: en:enba.*

24: en:enba.*

25: en:enba.*

26: en:enba.*

27: en:enba.*

28: en:enba.*

29: en:enba.*

30: en:enba.*

31: en:enba.*

32: en:enba.*

33: en:enba.*

34: en:enba.*

35: en:enba.*

36: en:enba.*

37: en:enba.*

38: en:enba.*

39: en:enba.*

40: en:enba.*

41: en:enba.*

42: en:enba.*

43: en:enba.*

44: en:enba.*

45: en:enba.*

Read No. is the number of results predicted by chance to have a score greater than or equal to the report of the best hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7 100.0	19 28	A2817238	2M0086001	
2	7 100.0	19 28	A2990856	2M0274F14	
3	7 100.0	22 28	A2623945	1M0462310	
4	7 100.0	22 28	A2591536	1M0354M17	

C 5	7 100.0	24 38	A2056679	1M0271135	
C 6	7 100.0	24 38	A2233817	1M0203219	
C 7	7 100.0	24 38	A2478673	1M0298320	
C 8	7 100.0	24 38	A2616657	2M0085805	
C 9	7 100.0	24 38	A2616657	2M0085805	
C 10	7 100.0	25 38	A2605844	1M047322	
C 11	7 100.0	25 38	A2802490	2M0061122	
C 12	7 100.0	25 38	BH52860	SAUK_0756	
C 13	7 100.0	25 38	BH52860	SAUK_0756	
C 14	7 100.0	25 38	BH52860	SAUK_0756	
C 15	7 100.0	26 38	A245685	1M008006	
C 16	7 100.0	26 38	A245685	1M008006	
C 17	7 100.0	26 38	A245685	1M008006	
C 18	7 100.0	26 38	A245685	1M008006	
C 19	7 100.0	26 38	A245685	1M008006	
C 20	7 100.0	26 38	A245685	1M008006	
C 21	7 100.0	26 38	A245685	1M008006	
C 22	7 100.0	26 38	A245685	1M008006	
C 23	7 100.0	26 38	A245685	1M008006	
C 24	7 100.0	26 38	A245685	1M008006	
C 25	7 100.0	26 38	A245685	1M008006	
C 26	6 85.7	16 12	BG598185	1M0367103	
C 27	6 85.7	17 12	BG598185	1M0367103	
C 28	6 85.7	17 12	BG598185	1M0367103	
C 29	6 85.7	17 12	BG598185	1M0367103	
C 30	6 85.7	17 12	BG598185	1M0367103	
C 31	6 85.7	17 12	BG598185	1M0367103	
C 32	6 85.7	17 12	BG598185	1M0367103	
C 33	6 85.7	17 12	BG598185	1M0367103	
C 34	6 85.7	17 12	BG598185	1M0367103	
C 35	6 85.7	17 12	BG598185	1M0367103	
C 36	6 85.7	17 12	BG598185	1M0367103	
C 37	6 85.7	17 12	BG598185	1M0367103	
C 38	6 85.7	17 12	BG598185	1M0367103	
C 39	6 85.7	17 12	BG598185	1M0367103	
C 40	6 85.7	17 12	BG598185	1M0367103	
C 41	6 85.7	17 12	BG598185	1M0367103	
C 42	6 85.7	17 12	BG598185	1M0367103	
C 43	6 85.7	17 12	BG598185	1M0367103	
C 44	6 85.7	17 12	BG598185	1M0367103	
C 45	6 85.7	17 12	BG598185	1M0367103	

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M02D00077214-A2.
21-DEC-2000.
14-JUN-2000; 2000M0-USI62233.
16-JUN-1999; 99US-O335032.

(UYCO) UNIV JOHNS HOPKINS.
Velculescu V, Vogelstein B, Kinzler K;
WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis
of gene expression (SAGE) tags, useful for studying, monitoring and
affecting phases of the cell cycle -

The present invention describes an isolated RNA molecule, comprising a
coding sequence of a yeast gene selected from a group of 745 NORFs not
previously assigned open reading frame; or nonannotated ORF) genes
comprising a SAGE serial analysis of gene expression) tag. Also,
the present invention provides a method for identifying candidate drug
cycles comprising administering a NORF gene whose expression varies by at
least 10 between any two phases of the cell cycle selected from log
phase lag and G2/M4 (2). The method (a) for screening candidate
phases of the cell cycle comprises:
yeast cell; and (b) monitoring expression of a NORF gene whose
expression varies as in M4, where a test substance which modifies the
progression of the cell cycle is administered to the yeast cell.
(w1) for identifying putative drugs having a characteristic effect on
proliferation comprising contacting human DNA with a probe which comprises
at least 10 contiguous nucleotides of a NORF gene whose expression varies
by at least 10 between any two phases of the cell cycle selected from
log phase lag and G2/M4 (2).

A class of drugs having a characteristic effect on gene
expression in a yeast cell comprising contacting a yeast cell with a
candidate drug and monitoring expression in the yeast cell of at least 1
NORF gene whose expression varies by at least 10 between any two phases
of the differentially expressed genes may be used as markers of phases of
the cell cycle. These methods may be used to identify candidate drugs which
affect the cell cycle.
AAFC33568 to represent SAGE tags used in the exemplification of
the present invention. AAF33262 to AAF33267 represent linkers and PCR
primers used in the SAGE method, in the exemplification of the present
invention.

```

Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;

Query Match      100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. NO. 5.7e-04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

	QY	1 AGTATGA 7
	DB	3 AGTATGA 9
		RESULT 12
		AAD#4180
		AAD#4180 standard; DNA; 10 BP.
		XX XX AAD#4180;
		XX XX
		13-DEC-2002 (first entry)
	DT	Probe #3 used to illustrate the method of the invention.
	DE	Target nucleotide; analyte; signal; drug discovery; probe; ss.
	DG	
	DX	
	XW	

[illegible]

FH	Key	Location/Qualifiers
FT	modified base	1..10

PT DNA fragments useful for increasing p53 activity in a cell and reducing
XX susceptibility to UV-induced hyperproliferative diseases -
XX Claim 1: Page 30; 44pp; English.

CC AAS10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are used as UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC UV-irradiation and subsequent exposure to UV-irradiation. The oligonucleotides
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.7e+08; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 AGATAGA 7
Db 1 AGATAGA 7
|||||||

RESULT 2
AAS14907
AAS14907 standard; DNA; 7 BP.
AC AAS14907;
14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #3.
XX Melanin; melanogenic; oligomer; cytosolic; anti-allergic; p53;
XX anti-inflammation; dermatological; ophthalmological; anti-psoriatic;
XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
XX conjunctivitis; allergic rhinitis; vitiligo; as;
XX Synthetic.

XX NO200174342-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10162.
XX 31-MAR-2000; 2000US-0540843.
XX (UYBO-) UNIV BOSTON.
XX Gluchrest BA, Year M, Eller M;

XX WPI: 2001-626338/72.
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
XX ultra-violet light -
XX Claim 1: Page 36; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell
XX proliferation by using specific oligonucleotides that mimic the effects of
XX ultra-violet light. The compounds, which have cytosolic, anti-allergic,
XX anti-inflammation, dermatological, ophthalmological, anti-psoriatic and
XX immunosuppressive effects, are used for treating psoriasis, atopic dermatitis, allergic
XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX and reducing susceptibility to skin cancer. Probably they mimic products of
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53

CC pathway, resulting in transient arrest of cell growth, allowing more time
CC for DNA repair and subsequent apoptosis. The oligonucleotides are used
CC especially used to treat carcinoma but may also be used to treat other
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);
CC reduce photoaging and subsequent exposure to UV-irradiation; treat
CC allergic rhinitis and conjunctivitis; prevent or reduce DNA damage in
CC cells caused by radiation or chemicals; increase melanin production in
CC cells; promote apoptosis in epithelial cells that contain damaged DNA. Also
CC oligonucleotides that contain non-hydrolyzable backbones are used to
CC inhibit apoptosis, in response to DNA damage, in epithelial cells. This
CC version of the oligonucleotide shown in AAS14906, one of the structures
CC oligonucleotides used to inhibit mammalian epithelial cell
XX proliferation, described in the method of the invention.

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.7e+08; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 AGATAGA 7
Db 1 AGATAGA 7
|||||||

RESULT 3
AAS14911
AAS14911 standard; DNA; 7 BP.
AC AAS14911;
14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #7.
XX Melanin; melanogenic; oligomer; cytosolic; anti-allergic; p53;
XX anti-inflammation; dermatological; ophthalmological; anti-psoriatic;
XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
XX conjunctivitis; allergic rhinitis; vitiligo; as;
XX Synthetic.

XX Key Location/Qualifiers
XX modified_base 1
XX Page a
XX /mod_base= a
XX /note= *Phosphorylated*
XX NO200174342-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10162.
XX 31-MAR-2000; 2000US-0540843.
XX (UYBO-) UNIV BOSTON.
XX Gluchrest BA, Year M, Eller M;

XX WPI: 2001-626338/72.
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
XX ultra-violet light -
XX Claim 1: Page 38; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell
XX proliferation by using specific oligonucleotides that mimic the effects of
XX ultra-violet light. The compounds, which have cytosolic, anti-allergic,
XX anti-inflammation, dermatological, ophthalmological, anti-psoriatic and
XX immunosuppressive effects, are used for treating psoriasis, atopic dermatitis, allergic
XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX and reducing susceptibility to skin cancer. Probably they mimic products of
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53

XX Query Match 100.0%; Score 7; DB 23; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 3.7e+08; Indels 0; Gaps 0;
XX Matches 7; Conservative 0; Mismatches 0;

XX Qy 1 AGATAGA 7
XX Db 1 AGATAGA 7
XX |||||||

XX RESULT 3
XX AAS14911
XX AAS14911 standard; DNA; 7 BP.
XX AC AAS14911;
XX 14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #7.
XX Melanin; melanogenic; oligomer; cytosolic; anti-allergic; p53;
XX anti-inflammation; dermatological; ophthalmological; anti-psoriatic;
XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
XX conjunctivitis; allergic rhinitis; vitiligo; as;
XX Synthetic.


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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GTATG 5
    Db 3 GTATG 7

RESULT 10
LOCUS AX667174/c
DEFINITION Sequence 623 from Patent WO242459.
ACCESSION AX667174.1 GI:29291326
VERSION 1
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
finger proteins
JOURNAL
PATENT WO 0242459-A 2256 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source
1..9
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:12630"
    /note="example target DNA"
BASE COUNT 2 a 2 c 3 g
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

1 GTATG 5
6 GTATG 2

RESULT 11
LOCUS AX668071
DEFINITION Sequence 2256 from Patent WO242459.
ACCESSION AX668071.1 GI:29291782
VERSION 1
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
finger proteins
JOURNAL
PATENT WO 0242459-A 2256 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source
1..9
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:12630"
    /note="example target DNA"
BASE COUNT 2 a 0 c 4 g
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

1 GTATG 5
4 GTATG 8

RESULT 12
LOCUS AX66807
DEFINITION Sequence 2256 from Patent WO242459.
ACCESSION AX668071.1 GI:29291782
VERSION 1
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
finger proteins
JOURNAL
PATENT WO 0242459-A 2256 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source
1..9
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:12630"
    /note="example target DNA"
BASE COUNT 2 a 0 c 4 g
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

1 GTATG 5
4 GTATG 8

RESULT 13
LOCUS SS0583
DEFINITION Type I procollagen [human, MENA Mutant, 9 nt].
ACCESSION SS0583
VERSION 1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 9)
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /note="example target DNA"
JOURNAL
MEDLINE
J91340689
PUBMED
1874719
REMARK
entry [NCBI gi|39475083] from the original journal article.
This sequence comes from Fig 5A.
FEATURES
source
1..9
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /note="example target DNA"
BASE COUNT 1 a 3 c 2 g
ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

1 GTATG 5
4 GTATG 8

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Copied from 09980559 on 05/19/2004

GenCore version 3.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21; Search time 144.494 Seconds
(without alignment)
93.410 Million cell updates/sec

Title: US-09-540-843-4

Perfect score: 5

Sequence: 1 gcatg 5

Scoring table: IDENTITY NUC

Gapop 10.0, Gapexc 1.0

Searched: 252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2101872

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Lacking first 45 summaries

Database:

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2: /SIDS1/gcdata/geneseq/geneq-embl/NA1981.DAT.*
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4: /SIDS1/gcdata/geneseq/geneq-embl/NA1983.DAT.*
5: /SIDS1/gcdata/geneseq/geneq-embl/NA1984.DAT.*
6: /SIDS1/gcdata/geneseq/geneq-embl/NA1985.DAT.*
7: /SIDS1/gcdata/geneseq/geneq-embl/NA1986.DAT.*
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9: /SIDS1/gcdata/geneseq/geneq-embl/NA1988.DAT.*
10: /SIDS1/gcdata/geneseq/geneq-embl/NA1989.DAT.*
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12: /SIDS1/gcdata/geneseq/geneq-embl/NA1991.DAT.*
13: /SIDS1/gcdata/geneseq/geneq-embl/NA1992.DAT.*
14: /SIDS1/gcdata/geneseq/geneq-embl/NA1993.DAT.*
15: /SIDS1/gcdata/geneseq/geneq-embl/NA1994.DAT.*
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17: /SIDS1/gcdata/geneseq/geneq-embl/NA1996.DAT.*
18: /SIDS1/gcdata/geneseq/geneq-embl/NA1997.DAT.*
19: /SIDS1/gcdata/geneseq/geneq-embl/NA1998.DAT.*
20: /SIDS1/gcdata/geneseq/geneq-embl/NA1999.DAT.*
21: /SIDS1/gcdata/geneseq/geneq-embl/NA2000.DAT.*
22: /SIDS1/gcdata/geneseq/geneq-embl/NA2001A.DAT.*
23: /SIDS1/gcdata/geneseq/geneq-embl/NA2001B.DAT.*
24: /SIDS1/gcdata/geneseq/geneq-embl/NA2002.DAT.*
25: /SIDS1/gcdata/geneseq/geneq-embl/NA2003.DAT.*

Feat. No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	5	100.0	5	20	AAZ10695		Oligonucleotide se
2	5	100.0	5	20	AAZ10696		Oligonucleotide se
3	5	100.0	5	21	AAZ14908		Melanogenesis aso
4	5	100.0	5	21	AAZ14909		Melanogenesis aso
5	100.0	5	100.0	7	20	AAZ10694	Oligonucleotide se
6	5	100.0	7	23	AAZ14907		Melanogenesis aso
7	5	100.0	7	23	AAZ14908		Melanogenesis aso
8	5	100.0	8	22	AAZ09250		Direct repeat sequ

10 5 100.0 9 19 AAZ22360 A promoter regulat
11 5 100.0 9 19 AAZ22361 Gas complement gen
12 5 100.0 9 19 AAZ15899 Cyclin D transcript
13 5 100.0 9 20 AAZ10692 Oligonucleotide se
14 5 100.0 9 24 AAZ03786 Human RNA PCR pri
15 5 100.0 9 24 AAZ03786 Human RNA PCR pri
16 5 100.0 9 24 ABZ01504 Zinc finger protei
17 5 100.0 9 24 ABZ01504 Zinc finger protei
18 5 100.0 9 24 ABZ01504 Zinc finger protei
19 5 100.0 9 24 ABZ01504 Zinc finger protei
20 5 100.0 10 14 AAZ41164 Donor oligomer wit
21 5 100.0 10 15 AAZ01104 Merlin exon 14 spl
22 5 100.0 10 16 AAZ42425 Anticancer duplex
23 5 100.0 10 17 AAZ35734 Primer E19 for v.d
24 5 100.0 10 18 AAZ66073 (dc-dAn). (dg-dT)n
25 5 100.0 10 19 AAZ05127 Yeast tag for addi
26 5 100.0 10 19 AAZ05127 Yeast tag for addi
27 5 100.0 10 19 AAZ05127 Yeast tag for addi
28 5 100.0 10 19 AAZ05127 Yeast tag for addi
29 5 100.0 10 19 AAZ35910 Primer used in RAP
30 5 100.0 10 20 AAZ18629 p53 serial analysi
31 5 100.0 10 20 AAZ18629 Chromophore contai
32 5 100.0 10 20 AAZ18629 Chromophore contai
33 5 100.0 10 21 AAZ47120 Human monocyte and
34 5 100.0 10 21 AAZ47120 Human monocyte and
35 5 100.0 10 21 AAZ47120 Human monocyte and
36 5 100.0 10 21 AAZ47120 Human monocyte and
37 5 100.0 10 21 AAZ47120 Human monocyte and
38 5 100.0 10 21 AAZ47120 Human monocyte and
39 5 100.0 10 21 AAZ47120 Human monocyte and
40 5 100.0 10 21 AAZ47120 Human monocyte and
41 5 100.0 10 21 AAZ47120 Human monocyte and
42 5 100.0 10 21 AAZ47120 Human monocyte and
43 5 100.0 10 21 AAZ47120 Human monocyte and
44 5 100.0 10 21 AAZ47120 Human monocyte and
45 5 100.0 10 21 AAZ47120 Human monocyte and

ALIGNMENTS

RESULT 1
AAZ10695
ID AAZ10695 standard; DNA, 5 BP.
AC AAZ10695;
XX AAZ10695;
DE 23-NOV-1999 (first entry)
DT Oligonucleotide sequence that increases p53 activity in a cell.
FF
XX p53 activity; UV mutagen; UV-irradiation; UV-induced dermatosis;
XX melanoma; melanoma; melanoma; melanoma; melanoma; melanoma;
XX atopic dermatitis; allergic rhinitis; conjunctivitis; photodermatosis;
XX skin cancer; ps.
XX Synthetic.
XX
XX GH2336157-A.
XX
XX 13-OCT-1999.
XX
XX 24-MAR-1999; 99GB-0006758.
XX
XX 26-MAR-1998; 98US-0048927.
XX
XX (UTBO-) UNIV BOSTON.
XX Gilchrist BA, Yaar M, Eller M;
XX WPT, 1999-54320/46.

Copied from 09980559 on 05/19/2004

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:59.09, Search time 571.494 Seconds
211,530 Million cell updates/sec

Title: us-09-540-843-4
Perfect score: 5
Sequence: 1 gtag 5

Scoring Table: Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 121523056 residues
Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0
Maximum DB seq length: 30
Post-processing: Minimum Match 0%
Lining first 45 summaries

Database:

- 1: EST.*.esthba.*
- 2: EST.*.esthbm.*
- 3: EST.*.esthbn.*
- 4: EST.*.esthbn.*
- 5: EST.*.esthbn.*
- 6: EST.*.esthbn.*
- 7: EST.*.esthbn.*
- 8: EST.*.esthbn.*
- 9: EST.*.esthbn.*
- 10: EST.*.esthbn.*
- 11: EST.*.esthbn.*
- 12: EST.*.esthbn.*
- 13: EST.*.esthbn.*
- 14: EST.*.esthbn.*
- 15: EST.*.esthbn.*
- 16: EST.*.esthbn.*
- 17: EST.*.esthbn.*
- 18: EST.*.esthbn.*
- 19: EST.*.esthbn.*
- 20: EST.*.esthbn.*
- 21: EST.*.esthbn.*
- 22: EST.*.esthbn.*
- 23: EST.*.esthbn.*
- 24: EST.*.esthbn.*
- 25: EST.*.esthbn.*
- 26: EST.*.esthbn.*
- 27: EST.*.esthbn.*
- 28: EST.*.esthbn.*
- 29: EST.*.esthbn.*
- 30: EST.*.esthbn.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Score	Query	Description
No.	Match	Length	DB ID
C 1	5 100.0	14 12	BM98220
C 2	5 100.0	16 9	AI24037
C 3	5 100.0	16 9	AI685758
C 4	5 100.0	16 9	AI721735

C 5	5 100.0	16 12	BM982185
C 6	5 100.0	17 12	BM982060
C 7	5 100.0	17 13	BM985683
C 8	5 100.0	17 14	BM985683
C 9	5 100.0	17 14	BM985683
C 10	5 100.0	19 9	BM987115
C 11	5 100.0	19 9	BM987115
C 12	5 100.0	19 9	BM987115
C 13	5 100.0	19 9	BM987115
C 14	5 100.0	19 9	BM987115
C 15	5 100.0	19 9	BM987115
C 16	5 100.0	19 9	BM987115
C 17	5 100.0	19 9	BM987115
C 18	5 100.0	19 9	BM987115
C 19	5 100.0	19 9	BM987115
C 20	5 100.0	19 9	BM987115
C 21	5 100.0	19 9	BM987115
C 22	5 100.0	19 9	BM987115
C 23	5 100.0	19 9	BM987115
C 24	5 100.0	19 9	BM987115
C 25	5 100.0	19 9	BM987115
C 26	5 100.0	19 9	BM987115
C 27	5 100.0	19 9	BM987115
C 28	5 100.0	19 9	BM987115
C 29	5 100.0	19 9	BM987115
C 30	5 100.0	19 9	BM987115
C 31	5 100.0	19 9	BM987115
C 32	5 100.0	19 9	BM987115
C 33	5 100.0	19 9	BM987115
C 34	5 100.0	19 9	BM987115
C 35	5 100.0	19 9	BM987115
C 36	5 100.0	19 9	BM987115
C 37	5 100.0	19 9	BM987115
C 38	5 100.0	19 9	BM987115
C 39	5 100.0	19 9	BM987115
C 40	5 100.0	19 9	BM987115
C 41	5 100.0	19 9	BM987115
C 42	5 100.0	19 9	BM987115
C 43	5 100.0	19 9	BM987115
C 44	5 100.0	19 9	BM987115
C 45	5 100.0	19 9	BM987115

ALIGNMENTS

BM98220 - 011.1 Chlous 14 bp MNNA linear EST 17-JAN-2002
LOCUS: BM98220.1
DEFINITION: Tetrahymena thermophila cDNA, MNNA sequence.
ACCESSION: BM98220.1
VERSION: 1
KEYWORDS: Tetrahymena thermophila
SOURCE: Tetrahymena thermophila
ORGANISM: Tetrahymena thermophila
REFERENCE: 1 (bases 1 to 14) Tetrahymena, Tetrahymena.
AUTHORS: Turkewitz, A.P., Karer, K.M., Jain, C., Orlas, E., Kirk, K.E., Frankel, R. and Lobuchew, I.
TITLES: Tetrahymena thermophila, strain CU420.1, growing cells
JOURNAL: Unpublished
COMMENT: Contact: Turkewitz AP
University of Chicago and Cell Biology
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 4374
Email: aturkewitz@uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..14

BM982185 MNNA linear EST 17-JAN-2002
LOCUS: BM982185.1
DEFINITION: Tetrahymena thermophila cDNA, MNNA sequence.
ACCESSION: BM982185.1
VERSION: 1
KEYWORDS: Tetrahymena thermophila
SOURCE: Tetrahymena thermophila
ORGANISM: Tetrahymena thermophila
REFERENCE: 1 (bases 1 to 14) Tetrahymena, Tetrahymena.
AUTHORS: Turkewitz, A.P., Karer, K.M., Jain, C., Orlas, E., Kirk, K.E., Frankel, R. and Lobuchew, I.
TITLES: Tetrahymena thermophila, strain CU420.1, growing cells
JOURNAL: Unpublished
COMMENT: Contact: Turkewitz AP
University of Chicago and Cell Biology
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 4374
Email: aturkewitz@uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..14


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Db
14 GTATG 18

RESULT 14
A2341880
LOCUS A2341880
DEFINITION A2341880 Mouse 10kb plasmid UGUC1M library Mus musculus genomic
clone UGUC1M074004 R, genomic survey sequence.
A2341880
VERSION A2341880.1
KEYWORDS A2341880.1 GI:10418570
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
M. Rose,M., Rhee,R., Schmitt,M., Meenen,A., Pedersen,T., Reilly
and Wright,D., Weiser,R., Stokes,R., Tingeve,A., von Nieschusen,A.
Mouse whole genome scaffolding with paired end reads from 10kb
unpublished
JOURNAL
COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84132, USA
Tel.: 801 585 5106
Fax: 801 585 5106
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Size: 10074
Seq: CACACGAGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
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/mol_type="genomic DNA"
/submitter="JGI"
/db_xref="taxon:10090"
/clone="UGUC1M074004"
/sex="Male"
/clone_lib="Mouse 10kb plasmid UGUC1M library"
/node="vector: PMW42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant viscosity. The sheared DNA
was ligated to the blunt ends in high molar excess. The
polynucleotide kinase, Adaptor oligonucleotides were
added to the blunt ends in high molar excess. The
sheared DNA blunt ends were ligated for 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (G1472114|gb|p42907.1), a copy-number ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA and transformed into competent cells
and selected for ampicillin resistance."
BASE COUNT 4 a 4 c 6 g 5 t
ORIGIN
Query Match 100.0%; Score 5; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY
8 GTATG 12

RESULT 15
A2345849/c
LOCUS A2345849
DEFINITION A2345849 Mouse 10kb plasmid UGUC1M library Mus musculus genomic
clone UGUC1M0808D16 R, genomic survey sequence.
A2345849
VERSION A2345849.1
KEYWORDS A2345849.1 GI:10425066
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
M. Rose,M., Rhee,R., Schmitt,M., Meenen,A., Pedersen,T., Reilly
and Wright,D., Weiser,R., Stokes,R., Tingeve,A., von Nieschusen,A.
Mouse whole genome scaffolding with paired end reads from 10kb
unpublished
JOURNAL
COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84132, USA
Tel.: 801 585 5106
Fax: 801 585 5106
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Size: 10074
Seq: CACACGAGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/submitter="JGI"
/db_xref="taxon:10090"
/clone="UGUC1M0808D16"
/sex="Male"
/clone_lib="Mouse 10kb plasmid UGUC1M library"
/node="vector: PMW42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant viscosity. The sheared DNA
was ligated to the blunt ends in high molar excess. The
polynucleotide kinase, Adaptor oligonucleotides were
added to the blunt ends in high molar excess. The
sheared DNA blunt ends were ligated for 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (G1472114|gb|p42907.1), a copy-number ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA and transformed into competent cells
and selected for ampicillin resistance."
BASE COUNT 9 a 4 c 0 g 6 t
ORIGIN
Query Match 100.0%; Score 5; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Ov 1 GPATC 5
Db 13 GPATC 9
|||||

Search completed: December 31, 2003, 19:41:20
Job time : 578.494 secs

GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00, Search time 58.9311 Seconds
(without alignment)
296.096 Million cell updates/sec

Title: US-09-540-843-4

Perfect score: 5

Sequence: 1 GATG 5

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2263443 seqs, 170637950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Minimum 45 summaries

Listing first 45 summaries

Database:

- 1: /cgn2_6/prodata/1/pubna/US07_PUBCOMB.seq*
- 2: /cgn2_6/prodata/1/pubna/US08_PUBCOMB.seq*
- 3: /cgn2_6/prodata/1/pubna/US09_PUBCOMB.seq*
- 4: /cgn2_6/prodata/1/pubna/US10_PUBCOMB.seq*
- 5: /cgn2_6/prodata/1/pubna/US11_PUBCOMB.seq*
- 6: /cgn2_6/prodata/1/pubna/US12_PUBCOMB.seq*
- 7: /cgn2_6/prodata/1/pubna/US13_PUBCOMB.seq*
- 8: /cgn2_6/prodata/1/pubna/US14_PUBCOMB.seq*
- 9: /cgn2_6/prodata/1/pubna/US15_PUBCOMB.seq*
- 10: /cgn2_6/prodata/1/pubna/US16_PUBCOMB.seq*
- 11: /cgn2_6/prodata/1/pubna/US17_PUBCOMB.seq*
- 12: /cgn2_6/prodata/1/pubna/US18_PUBCOMB.seq*
- 13: /cgn2_6/prodata/1/pubna/US19_PUBCOMB.seq*
- 14: /cgn2_6/prodata/1/pubna/US20_PUBCOMB.seq*
- 15: /cgn2_6/prodata/1/pubna/US21_PUBCOMB.seq*
- 16: /cgn2_6/prodata/1/pubna/US22_PUBCOMB.seq*
- 17: /cgn2_6/prodata/1/pubna/US23_PUBCOMB.seq*
- 18: /cgn2_6/prodata/1/pubna/US24_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5	100.0	5	US-10-122-630-4	Sequence 4, Appl
2	5	100.0	5	US-10-122-630-6	Sequence 6, Appl
3	5	100.0	5	US-10-122-630-7	Sequence 7, Appl
4	5	100.0	5	US-10-122-630-8	Sequence 8, Appl
5	5	100.0	7	US-10-077-632-178023	Sequence 178023
6	5	100.0	7	US-10-077-632-178043	Sequence 178043
7	5	100.0	7	US-10-077-632-178043	Sequence 178043
8	5	100.0	7	US-10-122-630-3	Sequence 3, Appl
9	5	100.0	7	US-10-122-630-4	Sequence 4, Appl
10	5	100.0	7	US-10-122-630-5	Sequence 5, Appl
11	5	100.0	7	US-10-122-630-6	Sequence 6, Appl
12	5	100.0	7	US-10-122-630-7	Sequence 7, Appl
13	5	100.0	8	US-09-142-593-1	Sequence 1, Appl
14	5	100.0	8	US-09-142-593-1	Sequence 1, Appl
15	5	100.0	8	US-09-142-593-1	Sequence 1, Appl

16	5	100.0	8	US-10-122-630-4	Sequence 4, Appl
17	5	100.0	8	US-10-122-630-5	Sequence 5, Appl
18	5	100.0	8	US-10-122-630-6	Sequence 6, Appl
19	5	100.0	8	US-10-122-630-7	Sequence 7, Appl
20	5	100.0	8	US-10-122-630-8	Sequence 8, Appl
21	5	100.0	9	US-09-989-785-623	Sequence 623, App
22	5	100.0	9	US-09-989-785-623	Sequence 623, App
23	5	100.0	9	US-09-989-785-623	Sequence 623, App
24	5	100.0	9	US-09-989-785-623	Sequence 623, App
25	5	100.0	9	US-09-989-785-623	Sequence 623, App
26	5	100.0	9	US-09-989-785-623	Sequence 623, App
27	5	100.0	9	US-09-989-785-623	Sequence 623, App
28	5	100.0	9	US-09-989-785-623	Sequence 623, App
29	5	100.0	9	US-09-989-785-623	Sequence 623, App
30	5	100.0	9	US-09-989-785-623	Sequence 623, App
31	5	100.0	9	US-09-989-785-623	Sequence 623, App
32	5	100.0	9	US-09-989-785-623	Sequence 623, App
33	5	100.0	9	US-09-989-785-623	Sequence 623, App
34	5	100.0	9	US-09-989-785-623	Sequence 623, App
35	5	100.0	9	US-09-989-785-623	Sequence 623, App
36	5	100.0	9	US-09-989-785-623	Sequence 623, App
37	5	100.0	9	US-09-989-785-623	Sequence 623, App
38	5	100.0	9	US-09-989-785-623	Sequence 623, App
39	5	100.0	9	US-09-989-785-623	Sequence 623, App
40	5	100.0	9	US-09-989-785-623	Sequence 623, App
41	5	100.0	10	US-09-962-602-7	Sequence 7, Appl
42	5	100.0	10	US-09-962-602-7	Sequence 7, Appl
43	5	100.0	10	US-09-962-602-7	Sequence 7, Appl
44	5	100.0	10	US-09-962-602-7	Sequence 7, Appl
45	5	100.0	10	US-09-962-602-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
Sequence 4, Application US/10122630
Sequence 4, Application US/10122630
GENERAL INFORMATION:
APPLICANT: Glitchest, Barbara A.
APPLICANT: Yeast, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
CURRENT FILING DATE: 2002-04-12
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/467,012
PRIOR APPLICATION NUMBER: US 09/467,012
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/467,012
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/540,843
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows version 4.0
SEQUENCE: 5
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-4

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 678.08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GTATG 5

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Db          |||||
            1 GTATG 5

RESULT 2
US-10-122-630-6/c
/ Sequence 6, Application US/1012630
/ Publication No. US2003032610A1
/ GENERAL INFORMATION:
/ APPLICANT: Glitchrest, Barbara A.
/ APPLICANT: Eller, Mark S.
/ APPLICANT: Year, Mina
/ TITLE OF INVENTION: Method to Inhibit Cell Growth Using
/ Oligonucleotides
/ FILE REFERENCE: 0054-1088-018
/ CURRENT APPLICATION NUMBER: US/10/122,630
/ PRIOR APPLICATION NUMBER: US 08/467,012
/ PRIOR FILING DATE: 1995-06-06/0896/08386
/ PRIOR FILING DATE: 1995-06-03
/ PRIOR APPLICATION NUMBER: US 09/048,927
/ PRIOR FILING DATE: 1998-03-26/09/540,843
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: PCT/US01/10162
/ PRIOR FILING DATE: 2001-03-30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 5
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6
/ Sequence 4, Application US/1012633
/ Publication No. US200303261A1
/ GENERAL INFORMATION:
/ APPLICANT: Glitchrest, Barbara A.
/ APPLICANT: Eller, Mark S.
/ APPLICANT: Year, Mina
/ TITLE OF INVENTION: Method to Inhibit Cell Growth Using
/ Oligonucleotides
/ FILE REFERENCE: 0054-1088-018
/ CURRENT APPLICATION NUMBER: US/10/122,633
/ PRIOR APPLICATION NUMBER: US 09/540,843
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: PCT/US01/10162
/ PRIOR FILING DATE: 2001-03-30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 5
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA Fragment

Query Match      100.0% Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
DB      5 GTATG 1

RESULT 3
US-10-122-633-4
/ Sequence 4, Application US/1012633
/ Publication No. US200303261A1
/ GENERAL INFORMATION:
/ APPLICANT: Glitchrest, Barbara A.
/ APPLICANT: Eller, Mark S.
/ APPLICANT: Year, Mina
/ TITLE OF INVENTION: Method to Inhibit Cell Growth Using
/ Oligonucleotides
/ FILE REFERENCE: 0054-1088-019
/ CURRENT FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 09/540,843
/ PRIOR FILING DATE: 2000-03-31/US01/10162
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 5
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA Fragment

Query Match      100.0% Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
DB      5 GTATG 1

RESULT 5
US-10-027-632-178029/c
/ Sequence 178029, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ Polymorphisms in the Human Genome
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-30
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-09-24
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 178025

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; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029
Query Match
  100.0%; Score 5; DB 13; Length 7;
  Best Local Similarity 100.0%; Pred. No. 4.8e+08; Indels 0; Gaps 0;
  Mismatches 0; Conservative 0; Mismatches 0;
Qy 1 GTATG 5
Db 5 GTATG 1

```

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RESULT 6
US-10-027-632-178043/c
Sequence 178043, Application US/10027632
Publication No. US20030204075a9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/157,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 125720
SOFTWARE: PseIsEQ for Windows Version 4.0
LENGTH: 7

```

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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178043
Query Match
  100.0%; Score 5; DB 13; Length 7;
  Best Local Similarity 100.0%; Pred. No. 4.8e+08; Indels 0; Gaps 0;
  Mismatches 0; Conservative 0; Mismatches 0;
Qy 1 GTATG 5
Db 5 GTATG 1

```

```

RESULT 7
US-10-027-632-178029/c
Sequence 178029, Application US/10027632
Publication No. US20030204075a9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218

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; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/136,358
; NUMBER OF SEQ ID NOS: 125720
; SOFTWARE: PseIsEQ for Windows Version 4.0
; SEQ ID NO 178029
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029

```

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Query Match
  100.0%; Score 5; DB 14; Length 7;
  Best Local Similarity 100.0%; Pred. No. 4.8e+08; Indels 0; Gaps 0;
  Mismatches 0; Conservative 0; Mismatches 0;
Qy 1 GTATG 5
Db 5 GTATG 1

```

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RESULT 8
US-10-027-632-178043/c
Sequence 178043, Application US/10027632
Publication No. US20030204075a9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome

```

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/157,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 125720
SOFTWARE: PseIsEQ for Windows Version 4.0
; SEQ ID NO 178043
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178043

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Query Match
  100.0%; Score 5; DB 14; Length 7;
  Best Local Similarity 100.0%; Pred. No. 4.8e+08; Indels 0; Gaps 0;
  Mismatches 0; Conservative 0; Mismatches 0;
Qy 1 GTATG 5
Db 5 GTATG 1

```

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RESULT 9
US-10-122-630-3
Sequence 3, Application US/10122630
Publication No. US20030032610A1
APPLICANT: Gluchrest, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Year, Mina

```

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/ TITLE OF INVENTION: Method to Inhibit Cell Growth Using
/ FILE REFERENCE: 0054.1088-018
/ CURRENT APPLICATION NUMBER: US/10/122.630
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: US 08/467,012
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: US 09/046,927
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: US 09/540,843
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: PCT/US01/10162
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 7
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-3
Query Match 100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0% Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GATC 5
|||||
2 GATC 6

```

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/ TITLE OF INVENTION: Method to Inhibit Cell Growth Using
/ FILE REFERENCE: 0054.1088-018
/ CURRENT APPLICATION NUMBER: US/10/122.630
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: US 08/467,012
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: US 09/046,927
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: US 09/540,843
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: PCT/US01/10162
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 7
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7
Query Match 100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0% Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GATC 5
|||||
2 GATC 6

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/ TITLE OF INVENTION: Method to Inhibit Cell Growth Using
/ FILE REFERENCE: 0054.1088-019
/ CURRENT APPLICATION NUMBER: US/10/122.633
/ PRIOR FILING DATE: 2002-03-31
/ PRIOR APPLICATION NUMBER: US 09/540,843
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: PCT/US01/10162
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 7
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3
Query Match 100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0% Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GATC 5
|||||
2 GATC 6

```

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/ TITLE OF INVENTION: Method to Inhibit Cell Growth Using
/ FILE REFERENCE: 0054.1088-018
/ CURRENT APPLICATION NUMBER: US/10/122.633
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: US 08/467,012
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: US 09/046,927
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: US 09/540,843
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: PCT/US01/10162
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 7
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7
Query Match 100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0% Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GATC 5
|||||
2 GATC 6

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1 FILE REFERENCE: STAM-160C1P
2 CURRENT APPLICATION NUMBER: US/09/927.886
3 PRIORITY FILING DATE: 2001-05-19
4 PRIOR APPLICATION NUMBER: 60/142,279
5 PRIOR FILING DATE: 1999-10-28
6 PRIOR APPLICATION NUMBER: 09/440,301
7 PRIORITY FILING DATE: 2001-05-11-17
8 NUMBER OF SEQ ID NOS: 19
9 SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 17
11 NAME:
12 TYPE: DNA
13 ORGANISM: Artificial Sequence
14 PATENT INFORMATION: transposon repeat sequence
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DEFINITION Sequence 11 from patent US 5856096.
ACCESSION AR026486
VERSION AR026486.1 GI:5937326
KEYWORDS
SOURCE Unknown.
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REFERENCE 1 (bases 1 to 11)
AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
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ACCESSION AR026487
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TITLE Rapid and sensitive assays for detecting and distinguishing between
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DEFINITION Sequence 2 from patent US 5837857.
ACCESSION AR055195
VERSION AR055195.1 GI:5984772
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 2 17-NOV-1998;
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DEFINITION Sequence 3 from patent US 5958680.
ACCESSION AR075506
VERSION AR075506.1 GI:10002256
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Vilponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 3 28-SEP-1999;
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ACCESSION AR161904
VERSION AR161904.1 GI:16228913
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Vilponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 2 10-JUL-2001;

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DEFINITION AR306454
ACCESSION AR306454
VERSION AR306454.1 GI:31694293
KEYWORDS
UNCLASSIFIED
ORGANISM
Unclassified.
REFERENCE Villaseca J, Pank W, and Andrews W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6548298-A 2 15-APR-2003;
FEATURES Location/Qualifiers
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ACCESSION AX033373
VERSION AX033373.1 GI:10280147
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE Eukaryotes; Metazoa; Chordata; Crustacea; Vertebrata; Rutelescomli,
TITLE Eukaryotes; Metazoa; Chordata; Crustacea; Vertebrata; Rutelescomli,
JOURNAL Mammalia; Rutelescomli; Primates; Catarrhini; Homiidae; Homo.
LARSSEN FRANK (NO) ; SKAANSING MARIANNE (NO)
Patent: WO 0046601-A 5 10-AUG-2000;
Detecting telomerase activity
KEYWORDS LARSSEN FRANK (NO) ; SKAANSING MARIANNE (NO)
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DEFINITION Sequence 5 from Patent WO0174342.
ACCESSION AX268757
VERSION AX268757.1 GI:16541829
KEYWORDS
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artificial sequences.
REFERENCE Gluchrest R.A., Yarr M. and Eller M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 5 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES Location/Qualifiers
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DEFINITION Sequence 9 from Patent WO0174342.
ACCESSION AX268761
VERSION AX268761.1 GI:16541833
KEYWORDS
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ORGANISM
artificial sequences.
REFERENCE Gluchrest R.A., Yarr M. and Eller M.
TITLE Use of locally applied dna fragments
JOURNAL Patent: WO 0174342-A 9 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
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RESULT 11
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LOCUS AX262236 11 bp DNA linear PAT 20-NOV-2001

Copied from 09980359 on 05/19/2004


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REFERENCE
AUTHORS Shay,J.W., Wright,M.E., Pietysek,M.A., Corey,D. and Norton,J.C.
TITLE Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL Nucleic Acids Res 200151:7929-A 43 09-OCT-2001;
COMMENT GS Identical: 2001517929-A 43 09-OCT-2001;
OS Unidentified
PR JP 2001517929-A/43
PR JP 2001517929-A/43
PR 09-APR-1997 JP 1997536487
PR 09-APR-1997 US 08/630019
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PI JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
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LOCUS BD176143 11 bp RNA linear PAT 18-MAR-2003
DEFINITION Mammalian telomerase.
ACCESSION BD176143
VERSION 1
KEYWORDS JP 2002272489-A/2.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,M. and Andrews,W.H.
JOURNAL J Biol Chem 2002272489-A 2 24-SEP-2002;
COMMENT GS Identical: 2002272489-A 2 24-SEP-2002;
OS Unidentified
PR 24-SEP-2002
PR 06-MAR-2002 JP 2002961125
PR 06-MAR-2002 US 08/272102,27-OCT-1994 US 08/316123 PR
PR JUD-1994 US 08/272102,27-OCT-1994 US 08/316123 PR
PR VILLEPONTEAU JUNLI FENG, WALTER FUNK, WILLIAM H ANDREWS PC
C12M15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
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Job time : 104.7 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 Search time 317.886 Seconds
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Title: US-09-540-843-5

Perfect score: 1 gtaggattag 11

Sequences: IDENTITY NUC

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Listing first 45 summaries

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ALIGNMENTS

RESULT 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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Feat. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

XX ANJ26728;
 XX 26-NOV-2001 (first entry)
 XX Phosphoramidate-linked 2'-arabino-fluoroligonucleotide.
 DE 2'-arabino-fluoroligonucleotide; phosphoramidate; telomerase;
 XX inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
 XX virus; antineoplastic; antigen; antigen; antigen; antigen;
 XX Synthetic.
 XX Key Location/Qualifiers
 XX modified_base 2..11
 XX /mod_base="OTHER"
 XX /note="2'-arabino-fluoroligonucleotides"
 XX modified_base 11..11
 XX /mod_base="OTHER"
 XX /note="phosphoramidate linkage"
 XX MO200153307-AL
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001MO-US01918.
 XX 21-JAN-2000; 2000US-178248P.
 XX (GERO-) GERON CORP.
 XX Gryanov S. Schultz RG;
 XX WPI; 2001-589652/66.
 XX Polynucleotides used to detect and isolate nucleic acids, inhibit
 XX function of RNA and telomerase enzymes and to treat e.g. viral
 XX infections, contain 2'-arabino-fluoroligonucleoside(s) linked to
 XX nucleoside(s) -
 XX Example 6; Page 46; 61pp; English.
 XX The present sequence is that of a N3'-P5' 2'-arabino-fluoro
 XX telomerase RNA. The oligonucleotide was used to assess the
 XX relative efficacy of novel 2'-arabino-fluoro phosphoramidate
 XX oligonucleotides and their 2'-ribo fluoroligonucleotide
 XX counterparts (see ANJ26728-25) for the inhibition of telomerase
 XX activity. Novel phosphoramidate 2'-arabino-fluoroligonucleotides
 XX are generally more acid stable, more resistant to cellular
 XX processes, and also show greater telomerase inhibition activity
 XX for treating cancer (claimed) and other diseases in which telomerase
 XX activity is present at abnormal levels, such as hyperproliferative
 XX disease (e.g. psoriasis, rheumatoid arthritis, cancer).
 XX immunosuppressive disorders, such as HIV/AIDS, and in the
 XX treatment of viral infection (claimed).
 XX Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GTTAGGCTTAG 11
 Db 1 GTTAGGCTTAG 11

RESULT 12
 ANJ26732

XX ANJ26732 standard, DNA, 11 BP.
 XX ANJ26732;
 XX 26-NOV-2001 (first entry)
 XX Phosphoramidate-linked 2'-ribose-fluoroligonucleotide.
 DE 2'-ribose-fluoroligonucleotide; phosphoramidate; telomerase;
 XX inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
 XX virus; antineoplastic; antigen; antigen; antigen; antigen;
 XX Synthetic.
 XX Key Location/Qualifiers
 XX modified_base 1..11
 XX /mod_base="OTHER"
 XX /note="2'-ribose-fluoroligonucleotides"
 XX modified_base 11..11
 XX /mod_base="OTHER"
 XX /note="phosphoramidate linkage"
 XX MO200153307-AL
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001MO-US01918.
 XX 21-JAN-2000; 2000US-178248P.
 XX (GERO-) GERON CORP.
 XX Gryanov S. Schultz RG;
 XX WPI; 2001-589652/66.
 XX Polynucleotides used to detect and isolate nucleic acids, inhibit
 XX function of RNA and telomerase enzymes and to treat e.g. viral
 XX infections, contain 2'-arabino-fluoroligonucleoside(s) linked to
 XX nucleoside(s) -
 XX Example 6; Page 46; 61pp; English.
 XX The present sequence is that of a 2'-ribose-fluoro
 XX telomerase RNA. The oligonucleotide was used to assess the
 XX relative efficacy of novel 2'-arabino-fluoro phosphoramidate
 XX oligonucleotides and their 2'-ribo fluoroligonucleotide
 XX counterparts (see ANJ26728-25) for the inhibition of telomerase
 XX activity. Novel phosphoramidate 2'-arabino-fluoroligonucleotides
 XX are generally more acid stable, more resistant to cellular
 XX processes, and also show greater telomerase inhibition activity
 XX for treating cancer (claimed) and other diseases in which telomerase
 XX activity is present at abnormal levels, such as hyperproliferative
 XX disease (e.g. psoriasis, rheumatoid arthritis, cancer).
 XX immunosuppressive disorders, such as HIV/AIDS, and in the
 XX treatment of viral infection (claimed).
 XX Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GTTAGGCTTAG 11
 Db 1 GTTAGGCTTAG 11

RESULT 13

AA514909
ID AA51909 standard; DNA; 11 BP.
XX
AC AA51909;
DT 14-FEB-2002 (first entry)
DE
KW Melanogenesis associated oligonucleotide #5.
KW melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
KW conjunctivitis; allergic rhinitis; vitiligo; se.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /*mod_base= g
XX /*note= "Optionally phosphorylated"
XX modified_base 2 /*tag= b
XX /*mod_base= OTHER
XX /*note= "OTHER= Optionally phosphorothiolate linkages"
XX WO200174342-A2.
XX
XX 11-OCT-2001.
XX 30-MAR-2001; 2001MO-US10162.
XX 31-MAR-2000; 2000US-0540843.
XX (UTBO-) UNIV BOSTON.
XX Gilchrist BA, Year M, Eller M.
XX WPI; 2001-626338/72.
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
XX ultra-violet light -
XX Claim 1; Page 37; 7app; English.
XX The invention describes inhibition of mammalian epithelial cell
XX proliferation by treating cells with at least one oligonucleotide, or
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce
XX radiation or chemical), as a proliferation inhibitor, apoptosis inducer
XX or a tumor necrosis factor inhibitor. Probably they mimic products of
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53
XX pathway, resulting in transient arrest of cell growth, allowing more time
XX for DNA repair to occur before cell division takes place. The method is
XX especially used to treat carcinoma but may also be used to: treat other
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);
XX anti-inflammatory mediated inflammation (atopic or contact dermatitis);
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo); and to
XX promote apoptosis in epithelial cells that contain damaged DNA. Also to
XX oligonucleotides that contain non-hydrolyzable backbones are used to
XX inhibit mammalian epithelial cell proliferation, described in the
XX method of the invention.

XX Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
XX Query Match 100.0%; Score 11; DB 23; Length 11;
XX Identical Similarity 100.0%; Identical Le-00; Indels 0; Gaps 0;
XX Mismatch 11; Conservative 0; Mismatches 0;
XX
XX Qy 1 OTTAGGTTAG 11
XX Db 1 OTTAGGTTAG 11
XX
XX RESULT 14
XX ID AA514913 standard; DNA; 11 BP.
XX AA514913;
XX 14-FEB-2002 (first entry)
XX Melanogenesis associated oligonucleotide #9.
XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX tumor necrosis factor inhibitor; photogingiv; hyperproliferative disease;
XX carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
XX conjunctivitis; allergic rhinitis; vitiligo; se.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /*mod_base= c
XX /*note= "Phosphorylated"
XX WO200174342-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001MO-US10162.
XX 31-MAR-2000; 2000US-0540843.
XX (UTBO-) UNIV BOSTON.
XX Gilchrist BA, Year M, Eller M.
XX WPI; 2001-626338/72.
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX carcinoma, using specific oligonucleotides that mimic the effects of
XX ultra-violet light -
XX Example 12; Page 37; 7app; English.
XX The invention describes inhibition of mammalian epithelial cell
XX proliferation by treating cells with at least one oligonucleotide, or
XX its fragment. The compounds, which have cytostatic, anti-allergic,
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce
XX DNA repair processes (or a protective response to later exposure to
XX radiation or chemical), as a proliferation inhibitor, apoptosis inducer
XX or a tumor necrosis factor inhibitor. Probably they mimic products of
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53
XX pathway, resulting in transient arrest of cell growth, allowing more time
XX for DNA repair to occur before cell division takes place. The method is
XX especially used to treat carcinoma but may also be used to: treat other
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);
XX anti-inflammatory mediated inflammation (atopic or contact dermatitis);
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo); and to
XX promote apoptosis in epithelial cells that contain damaged DNA. Also to
XX oligonucleotides that contain non-hydrolyzable backbones are used to
XX inhibit mammalian epithelial cell proliferation, described in the
XX method of the invention.

GenStore version 5.1.6
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OK nucleic - nucleic search, using sw model
Run on: December 31, 2003, 13:58:09, Search time 1820.89 Seconds
211,530 Million cell updates/sec

Title: US-09-540-843-5
Sequence: 1 gtagestag 11
Scoring table: IDENTITY, NUC
Gapop 10.0, Gapext 1.0

Searched: 2781392 seqs, 1215223056 residues
Total number of hits satisfying chosen parameters: 33330
Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

EST.* esrba.*
3: esrba.in.*
4: esrba.in.*
5: esrba.in.*
6: esrba.in.*
7: esrba.in.*
8: esrba.in.*
9: esrba.in.*
10: esrba.in.*
11: esrba.in.*
12: esrba.in.*
13: esrba.in.*
14: esrba.in.*
15: esrba.in.*
16: esrba.in.*
17: esrba.in.*
18: esrba.in.*
19: esrba.in.*
20: esrba.in.*
21: esrba.in.*
22: esrba.in.*
23: esrba.in.*
24: esrba.in.*
25: esrba.in.*
26: esrba.in.*
27: esrba.in.*
28: esrba.in.*
29: esrba.in.*

Result No. is the number of results predicted by chance to have a score as high as the one observed. Printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	19	28	A2614760
c 2	11	100.0	20	29	TA158A3P
c 3	11	100.0	25	29	TA158A3P
c 4	11	100.0	27	28	AB037795

5	9.4	85.5	23	28	A2614760
6	9.4	81.8	22	28	A2614760
7	9.9	81.8	22	14	D18745
8	9.9	81.8	24	28	BH077981
9	8.4	76.4	21	29	TA158A3P
10	8.4	76.4	24	29	TA158A3P
11	8.4	76.4	24	29	TA158A3P
12	8.4	76.4	24	29	TA158A3P
13	8.4	76.4	24	29	TA158A3P
14	8.4	76.4	24	29	TA158A3P
15	8.4	76.4	24	29	TA158A3P
16	8.4	76.4	24	29	TA158A3P
17	8.4	76.4	24	29	TA158A3P
18	8.4	76.4	24	29	TA158A3P
19	8.4	76.4	24	29	TA158A3P
20	8.4	76.4	24	29	TA158A3P
21	8.4	76.4	24	29	TA158A3P
22	8.4	76.4	24	29	TA158A3P
23	8.4	76.4	24	29	TA158A3P
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25	8.4	76.4	24	29	TA158A3P
26	8.4	76.4	24	29	TA158A3P
27	8.4	76.4	24	29	TA158A3P
28	8.4	76.4	24	29	TA158A3P
29	8.4	76.4	24	29	TA158A3P
30	8.4	76.4	24	29	TA158A3P
31	8.4	76.4	24	29	TA158A3P
32	8.4	76.4	24	29	TA158A3P
33	8.4	76.4	24	29	TA158A3P
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35	8.4	76.4	24	29	TA158A3P
36	8.4	76.4	24	29	TA158A3P
37	8.4	76.4	24	29	TA158A3P
38	8.4	76.4	24	29	TA158A3P
39	8.4	76.4	24	29	TA158A3P
40	8.4	76.4	24	29	TA158A3P
41	8.4	76.4	24	29	TA158A3P
42	8.4	76.4	24	29	TA158A3P
43	8.4	76.4	24	29	TA158A3P
44	8.4	76.4	24	29	TA158A3P
45	8.4	76.4	24	29	TA158A3P

RESULT 1	A2614760
LOCUS	A2614760 Mouse 10kb plasmid genomic clone U001M043A17 R, genomic survey sequence.
DEFINITION	A2614760.1 GI:11736950
ACCESSION	A2614760.1
VERSION	A2614760.1
KEYWORDS	Mouse whole genome scaffolding with paired end reads from 10kb
SOURCE	Mouse whole genome scaffolding with paired end reads from 10kb
ORGANISM	Mouse whole genome scaffolding with paired end reads from 10kb
REFERENCE	1 (bases 1 to 19)
AUTHORS	Dunn, D., Ayagi, A., Barber, M., Beaton, T., Duval, B., Hamil, C., Islam, H., Kongare, S., Mahmoud, M., Meenen, G., Pedersen, T., Kelly, and Wright, D. Weiser, R., Schaefer, A., Ling, A., von Niedermaier, A.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	PLoS ONE
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177

Email: damngene@vch.edu
 Title: Genomic survey sequence
 Seq primer: CACACGAGACACCTAGTACCC
 Cites: plasmid and genomic DNA
 High quality: yes
 Location/Qualifiers
 FEATURES
 source
 1..19
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10096"
 /sex="male"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_10b="Mouse 10b plasmid U9C1M library from Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/) The DNA was blunt end-repaired with T4 DNA polymerase and T4 ligase. The blunt end-repaired DNA was ligated into the blunt end-repaired plasmid. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was extracted from a derivative of pMD19 (G1173214) (pAT1092). The vector was ligated with adapters complementary to the insert adapters and the ligated DNA was transformed into competent cells. The adapted vector DNA and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 100.0%; Score 11; DB 29; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTAGGGTTAG 11
 Db 20 GTTAGGGTTAG 10

RESULT 3
 TTAGGGTTAG 1066
 LOCUS
 DEFINITION
 T. brucei sheared genomic DNA clone 15a03, forward sequence.
 ACCESSION
 AL472050.1
 VERSION
 AL472050.1 GI:11837404
 KEYWORDS
 Trypanosoma brucei
 SOURCE
 Trypanosoma brucei
 ORGANISM
 Trypanosoma
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma
 (Cases 1 to 20)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, P., Chillingworth, C., Omond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrall, B.G.
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barralle@sanger.ac.uk and Cambridge CB10 1SA. E-mail: barralle@sanger.ac.uk and Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRU927/4) (Gutart 10.1) was mechanically sheared into fragments of approximately 4 kb. The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Insert Libraries for Whole Genome Shotgun Sequencing Projects. In Barrall, Oxford University Press, 1999).
 Email: nelsayed@vch.org
 Details of vch brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 FEATURES
 source
 1..25
 /mol_type="genomic DNA"
 /strain="TRU927"
 /db_xref="taxon:5691"
 /clone_10b="15a03"
 BASE COUNT
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 ORIGIN
 Query Match 100.0%; Score 11; DB 29; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTAGGGTTAG 11
 Db 20 GTTAGGGTTAG 10

RESULT 3
 TTAGGGTTAG 1066
 LOCUS
 DEFINITION
 T. brucei sheared genomic DNA clone 15a03, forward sequence.
 ACCESSION
 AL472050.1
 VERSION
 AL472050.1 GI:11837404
 KEYWORDS
 Trypanosoma brucei
 SOURCE
 Trypanosoma brucei
 ORGANISM
 Trypanosoma
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma
 (Cases 1 to 20)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, P., Chillingworth, C., Omond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrall, B.G.
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barralle@sanger.ac.uk and Cambridge CB10 1SA. E-mail: barralle@sanger.ac.uk and Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRU927/4) (Gutart 10.1) was mechanically sheared into fragments of approximately 4 kb. The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Insert Libraries for Whole Genome Shotgun Sequencing Projects. In Barrall, Oxford University Press, 1999).
 Email: nelsayed@vch.org
 Details of vch brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 FEATURES
 source
 1..25
 /mol_type="genomic DNA"
 /strain="TRU927"
 /db_xref="taxon:5691"
 /clone_10b="15a03"
 BASE COUNT
 4 a 0 c 12 g
 ORIGIN
 Query Match 100.0%; Score 11; DB 29; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTAGGGTTAG 11
 Db 20 GTTAGGGTTAG 10

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGCTTAG 11
Db 4 GTTAGGCGTAG 14

RESULT 6
LOCUS D18745.7
DEFINITION Mus musculus domesticus (western European house mouse)
ACCESSION D18745.1 GI:1100714
VERSION 1
KEYWORDS EST, Mus musculus domesticus (western European house mouse)
ORGANISM Mus musculus domesticus
AUTHORS Fukuyama, M.; Metaxas, C.; Rodentia; Sciurognathi; Muridae; Eulacostroni;
REFERENCE Damm, D.; Ayres, J. A.; Barber, M.; Bascort, T.; Duvall, B.; Harlin, C.;
M. J. Rose, M.; Rose, R.; Stokes, R.; Tingey, A.; von Niederhausern, A.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished
COMMENT Contact: Kawasato, S., Okubo, K., Yoshi, J., Katsuki, M. and Matsubara
K. Institute for Cellular and Molecular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
Source
1..29
Location/Qualifiers
/organism="Mus musculus domesticus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/db_xref="taccdb:10092"
/clone="md1403"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
/clone="Mus musculus domesticus"
BASE COUNT 7 a 5 c 1 g
ORIGIN
Query Match 81.8%; Score 9; DB 14; Length 22;
Best local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTAGGCTTA 10
Db 21 TTAGGCTTA 13

RESULT 8
LOCUS BH077981/c
DEFINITION Arabidopsis thaliana genomic clone SALX-04-SBP-2002
ACCESSION BH077981.1 GI:22770914
VERSION 1
KEYWORDS GSS, Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
REFERENCE Alonso, J. M.; Leisner, T. J.; Barajas, P.; Chen, H.; Cheuk, R.; Gadrinab
C.; Jenkins, A.; Karsan, M.; Kim, C. J.; Parker, H. L.; Prednis, L.; Shim, P.
TITLE A Sequence-indexed Library of Insertion Mutations in the
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker


```

Sal Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 554 6339 x1752
Fax: 858 554 6339 x1752
Email: eckers@sigal.edu
This is single pass sequence recovered from the left border of
plasmid. The sequence is 118 within an annotated intron of AC194820.
Class: TUNA tagged
Location/Qualifiers
1..241=Arabidopsis thaliana"
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/strain="Columbia 0"
/ab_xref="taxon:320734.20"
/clone="pGEMT-320734.20"
/notes="PCR was performed on Arabidopsis thaliana lines
elements which contains one or more TUNA insertion
sites. The sequence was directly sequenced to determine the
site of insertion. Details of the protocols used can
be found at http://signal.sigal.edu/tdna_protocols.html"
BASE COUNT 11 a 2 c 2 5 6 c
ORIGIN
Query Match 81.0% Score 9. DB 28 Length 24;
Best Local Similarity 100.0%; Prot No 2, 26, 95; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
2 TTAGGGTTA 10
|||||||
12 TTAGGGTTA 4

RESULT 9
T196766315
196766315
DEFINITION
clone UGCLM561K14 R, genomic survey sequence.
ACCESSION
A2766315
VERSION
A2766315.1 GI:12893263
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
Organism
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1. (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C., Lilly
and Wright,D., Weis,R.,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Knight,D., Weis,R.
Mus musculus genome scaffolding with paired end reads from 10kb
plasmid libraries
CONTACT: Robert B. Weiss
University of Utah Health Science Center
Re: 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Phone: 801 586 5506
Fax: 801 585 7197
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Insert Start: 10000
Seq primer: GACGAGGAGACGACGATACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/retailer="CS961/65"

FEATURES
SOURCE
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"

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/strain="TREU927"
/clone="136c11.3691"
6 a 7 c 3 g 7 t

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 76.4%; Score 8.4; DS 29; Length 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 OTTAGGTTA 10
Db 23 OTTAGGTTA 14

RESULT 11
LOCUS A0256889 24 bp mRNA linear EST 25-APR-2002
DEFINITION A0256889 3'-directed mouse cDNA library Mus musculus cDNA clone
ACCESSION BE0009219 3', mRNA sequence.
VERSION A0256889.1 GI:20320970
XREFS
KEYWORDS EST.
ORIGIN Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kato, K and Mochi, R.
Generation of expressed sequence tags from mouse brain
Unpublished
COMMENT Submitted by: Kato,
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-73-72-5889
Fax: 81-73-72-5889
Email: kato@bs.aist-nara.ac.jp
URL: http://www.aist-nara.ac.jp/BS/BD/index.html.
FEATURES
source
1..24
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BE0009219"
/feature_type="Brain"
/clone="BD-3 3 g 5 t
10 a 6 c 3 g 5 t

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 76.4%; Score 8.4; DS 9; Length 24;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TTAGGGTTA 11
Db 15 TTAGGGTTA 6

RESULT 12
LOCUS AV544203 25 bp mRNA linear EST 07-SEP-2000
DEFINITION AV544203 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
ACCESSION AV544203.1 GI:9715617
XREFS EST.
KEYWORDS EST.
ORIGIN Arabidopsis thaliana (Chale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Eukaryota; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids
I; eurosid II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 25)

REFERENCE
1 (bases 1 to 25)
AUTHORS
Hail N., Bowman S., Lennard N.J., Doggett J., Atkin, E.,
Mannervik, G., Grind J., Karsberg, R., Hurrell, N., Hou, L.,
Mavill, M., Rispant, W. and Barrall, B.G.
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project. The Wellcome Trust, Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrall@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Hinxton, Cambridgeshire, UK. The genome of Trypanosoma
brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v. i. method used for the library construction is
described in the TIGR website. The library will be used to
insert libraries for whole genome shotgun sequencing projects. In
genome sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrall, Oxford University Press, 1999).
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
Location
/organism="Trypanosoma brucei"
/feature_type="genomic DNA"
/strain="TREU927"

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/db_xref="taxon:5691"
/cdname="274g11"

BASE COUNT      5 a      6 c      10 g      4 t
ORIGIN
Query Match      76.4%; Score 8.4; DB 29; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  2 TTAGGGTTAG 11
Db  18 TTAGGGTCG 9

RESULT 14
ACCESSION      AU25344
DEFINITION      AU25344.3-directed mouse cDNA library Mus musculus cDNA clone
VERSION      AU25344.1 GI:2031795
KEYWORDS      EST, musculus (house mouse)
ORGANISM      Mus musculus
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
PUBLISHED      Kato K. and Matsuda R.
JOURNAL      Unpublished
REFERENCE      Generation of expressed sequence tags from mouse brain
      Graduate School of Biological Sciences
      Nara Institute of Science and Technology
      891-5 Takayama, Ikoma, Nara 630-0101, Japan
      Tel: 81-743-72-5555
      Fax: 81-743-72-5589
      Email: kkatobba.aist-nara.ac.jp,
      URL: http://fore2.aist-nara.ac.jp/BED/index.html.

FEATURES
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     1..27
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     /organism="Mus musculus"
     /db_xref="taxon:10990"
     /clone="BED005210"
     /cldname_type="brain"
     /clone="3-directed mouse cDNA library"
BASE COUNT      11 a      5 c      3 g      8 t
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Query Match      76.4%; Score 8.4; DB 9; Length 27;
Best Local Similarity 90.0%; Pred. No. 5.5e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  2 TTAGGGTTAG 11
Db  19 TTAGGATTAG 10

TITLE      and Caskey, C.T.H.
JOURNAL      Isolation of chromosome-specific genes by reciprocal probing of
PUBLISHED      Hum. Mol. Genet. 4, 1373-1380 (1995)
COMMENT      7581376
FEATURES
     source
     location: GenQualifiers
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="XP256A"
     /clone_lib="Human placenta"
     /clone="1287.49 sec"
BASE COUNT      13 a      7 c      6 g      1 t
ORIGIN
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Best Local Similarity 90.0%; Pred. No. 5.5e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  2 TTAGGGTTAG 11
Db  19 TTGGGGTTAG 10

Search completed: December 31, 2003, 19:41:24
Job time : 1267.49 secs

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[illegible]

Query Match	100.0%;	Score 11;	DB 1;	Length 11;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		

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Query Match      100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 OTTAGGTTAG 11
 Db 11 OTTAGGTTAG 1

 RESULT 2
 US-08-482-1158-2/c
 ; Sequence 2, Application US/08482115B
 ; General Information:
 ; APPLICANT: Villeganteau, Bryant
 ; APPLICANT: Feng, Quail
 ; APPLICANT: Andrew, William H.
 ; TITLE OF INVENTION: Assays for the RNA Component of Human
 ; TITLE OF INVENTION: Assays for the RNA Component of Human
 ; NUMBER OF INVENTIONS: 1
 ; CORRESPONDENCE ADDRESS:
 ADDRESSES: Townsend and Townsend and Crew LLP
 ADDRESS: 2100 Subcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 POSTAL CODE: 94111-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/482.1158
 APPLICATION NUMBER: US/08/482.1158
 PRIORITY DATA: US/08/482.1158
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: US 08/272.102
 APPLICATION NUMBER: US 08/272.102
 FILING DATE: 17 OCT 1994
 PRIOR APPLICATION DATA: US 08/330.123
 APPLICATION NUMBER: US 08/330.123
 FILING DATE: 17 OCT 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 US-08-660-678A-2

 Query Match 100.0%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 OTTAGGTTAG 11
 Db 11 OTTAGGTTAG 1

RESULT 3
 US-08-660-678A-2/c
 ; Sequence 2, Application US/08660678A
 ; General Information:
 ; Patent No. 5837857
 ; APPLICANT: Villeganteau, Bryant
 ; APPLICANT: Feng, Quail
 ; APPLICANT: Funk, Walter
 ; APPLICANT: Andrew, William H.

; TITLE OF INVENTION: Mammalian Telomerase
 ; TITLE OF INVENTION: Mammalian Telomerase
 ; CORRESPONDENCE ADDRESS:
 ADDRESSES: Townsend and Townsend and Crew LLP
 ADDRESS: 2100 Subcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 POSTAL CODE: 94111-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/660.678A
 APPLICATION NUMBER: US/08/660.678A
 PRIORITY DATA: US/08/660.678A
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: US 08/330.123
 APPLICATION NUMBER: US 08/330.123
 FILING DATE: 17 OCT 1994
 PRIOR APPLICATION DATA: US 08/272.102
 APPLICATION NUMBER: US 08/272.102
 FILING DATE: 17 OCT 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 US-08-660-678A-2

 Query Match 100.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 OTTAGGTTAG 11
 Db 11 OTTAGGTTAG 1

 RESULT 4
 US-08-531-743-11
 ; Sequence 11, Application US/08531743
 ; Patent No. 5856096
 ; GENERAL INFORMATION:
 ; APPLICANT: Mindle, Bradford E.
 ; APPLICANT: Qiu, Ming
 ; APPLICANT: Chen, Shi-feng
 ; APPLICANT: Maimon, Ira
 ; APPLICANT: Maimon, Ira
 ; TITLE OF INVENTION: Rapid and Sensitive Assays for Detecting and
 ; TITLE OF INVENTION: Distinguishing Between Processive and
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ADDRESSES: Arnold, White & Durkee
 ADDRESS: P.O. Box 4133
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 POSTAL CODE: 21577-2100
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: 08/531,743
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 435
NAME: Hightower, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: CTRC:026/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGOGY: linear
US-08-531-743-11

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 GTTAGCGTTAG 11
Db 11 GTTAGCGTTAG 11

RESULT 6
US-08-485-778-36/c
; Sequence 36, Application US/08485778
; Patent No. 5876979
; GENE: HUMAN GENE.
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Juhli
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Mouton, Jean-Pierre
; TITLE OF INVENTION: COMPOUND OF TETRAHYDRO
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS: Brook, Smith & Reynolds, P.C.
; STREET: Two Willetta Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: 08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/387,524
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA: US 08/330,123
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; APPLICATION NUMBER: US 08/272,102
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLGOGY: linear
US-08-485-778-36

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 GTTAGCGTTAG 11
Db 11 GTTAGCGTTAG 11

OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: 08/531,743
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 435
NAME: Hightower, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: CTRC:026/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGOGY: linear
US-08-531-743-12/c

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 GTTAGCGTTAG 11
Db 11 GTTAGCGTTAG 11

RESULT 5
US-08-531-743-12/c
; Sequence 12, Application US/08531743
; Patent No. 5850960
; GENE: HUMAN GENE.
; APPLICANT: Windle, Bradford E.
; APPLICANT: Qiu, Ming
; APPLICANT: Chen, Shi-fong
; APPLICANT: Fung, Yung
; APPLICANT: Maize, Ira
; APPLICANT: Maize, Ira
; TITLE OF INVENTION: Rapid and Sensitive Assays for Detecting and
; Identifying Binding Between
; TITLE OF INVENTION: NO. 5050960-20030808 TELMORSE ARCHIVIS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: 08/531,743
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,743
; ATTORNEY/AGENT INFORMATION:
; NAME: Highland, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: CTRC:026/HYL
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLGOGY: linear

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CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/630,019A
 FILING DATE: 09-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid (RNA)
 DESCRIPTION: where (deoxy)ribosephosphate linkages are replaced by (2'-aminoethyl)glycine units linked to nucleotide bases via
 DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
 US-09-540-843-5

Query Match 100.0%; Score 11; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 0;

1 GTTAGGGTTAG 11
 1 GTTAGGGTTAG 11

RESULT 10
 Sequence 30, Application US/08630019A
 Patent No. 6015710
 GENERAL INFORMATION:
 APPLICANT: Shaw, Jerry W.
 APPLICANT: Wright, Woodring E.
 APPLICANT: Platyzek, Mieczyslaw A.
 APPLICANT: No. 6015710cn, James C.
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by
 TITLE OF INVENTION: Peptide Nucleic Acid
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/630,019A
 FILING DATE: 09-JUN-1996
 CLASSIFICATION: 516
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 US-09-540-019A-30

Query Match 100.0%; Score 11; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Gaps 0;
 Matches 11; Conservative 0; Indels 0;

Qy 1 GTTAGGGTTAG 11
 Db 11 GTTAGGGTTAG 11

RESULT 11
 Sequence 39, Application US/08630019A
 Patent No. 6015710
 GENERAL INFORMATION:
 APPLICANT: Jerry W.
 APPLICANT: Wright, Woodring E.
 APPLICANT: Platyzek, Mieczyslaw A.
 APPLICANT: No. 6015710cn, James C.
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by
 TITLE OF INVENTION: Peptide Nucleic Acids
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/630,019A
 FILING DATE: 09-JUN-1996
 CLASSIFICATION: 516
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: where (deoxy)ribosephosphate linkages are replaced by (2'-aminoethyl)glycine units linked to nucleotide bases via
 DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
 US-09-540-019A-39

Query Match 100.0%; Score 11; DB 3; Length 11;
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 Matches 11; Conservative 0; Indels 0;

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 Db 11 GTTAGGGTTAG 11

RESULT 12
 Sequence 43, Application US/08939545
 Patent No. 6046307

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 469.316 Seconds
 444.364 Million cell updates/sec

Title: US-09-540-843-6

Sequence: 1 catc 5

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Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: gb-hg-hum*

4: gb-hg-hum*

5: gb-hg-hum*

6: gb-hg-hum*

7: gb-hg-hum*

8: gb-hg-hum*

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10: gb-hg-hum*

11: gb-hg-hum*

12: gb-hg-hum*

13: gb-hg-hum*

14: gb-hg-hum*

15: gb-hg-hum*

16: gb-hg-hum*

17: gb-hg-hum*

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20: gb-hg-hum*

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22: gb-hg-hum*

23: gb-hg-hum*

24: gb-hg-hum*

25: gb-hg-hum*

26: gb-hg-hum*

27: gb-hg-hum*

28: gb-hg-hum*

29: gb-hg-hum*

30: gb-hg-hum*

31: gb-hg-hum*

32: gb-hg-hum*

33: gb-hg-hum*

34: gb-hg-hum*

35: gb-hg-hum*

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43: gb-hg-hum*

44: gb-hg-hum*

45: gb-hg-hum*

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 and is derived by analysis of the total score distribution."

SUMMARIES

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C	5	5	100.0	8	6	AZ68755	Sequence	AZ68755 Sequence
C	6	5	100.0	8	6	AZ68755	Sequence	AZ68755 Sequence
C	7	5	100.0	8	6	AZ68755	Sequence	AZ68755 Sequence
C	8	5	100.0	8	6	AZ68755	Sequence	AZ68755 Sequence
C	9	5	100.0	8	6	AZ68755	Sequence	AZ68755 Sequence
C	10	5	100.0	9	6	AZ68755	Sequence	AZ68755 Sequence
C	11	5	100.0	9	6	AZ68755	Sequence	AZ68755 Sequence
C	12	5	100.0	9	6	AZ68755	Sequence	AZ68755 Sequence
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C	14	5	100.0	9	6	AZ68755	Sequence	AZ68755 Sequence
C	15	5	100.0	9	6	AZ68755	Sequence	AZ68755 Sequence
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ALIGNMENTS

RESULT 1
 AZ68756/c
 DEFINITION Sequence 4 from Patent WO0174312.
 ACCESSION AZ68756
 VERSION AZ68756.1 GI:16541828
 SOURCE synthetic construct
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE Use of locally applied dna fragments
 Patent No. 0174312, filed Oct-2001;
 INVENTORS OF BOSTON UNIVERSITY (US)

linear PAT 29-OCT-2001

Pred. No. is the number of results predicted by chance to have a


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Oy 1 CACTAC 5
Db 2 CACTAC 6

RESULT 6
LOCUS AX104946 8 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1138 from Patent WO0122972.
ACCESSION AX104946
VERSION AX104946.1 GI:13921143
KEYWORDS
SOURCE synthetic construct
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 8)
AUTHORS Kriegl, A.M., Schetter, C. and Vollmer, J.C.
TITLE DNA-based transposon system for the introduction of nucleic acid
JOURNAL Patent WO 0122972-A1 136 05-1998-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Source Location/Qualifiers
BASE COUNT 2 a 1 c 2 g 3 t
Query Match 100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
LOCUS AX119567/c 8 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 224 from Patent WO0122951.
ACCESSION AX119567
VERSION AX119567.1 GI:14036486
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 8)
AUTHORS Sakayaka, T., Metacross, Chordates; Craniata; Vertebrates; Euteleostomi;
Mollusca; Mollusca; Primates; Catarrhini; Hominiidae; Homo.
Messiaen, L. and Callens, T.
TITLE Patented WO 0122951-A1 26-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Source Location/Qualifiers
BASE COUNT 1 a 0 c 4 g 3 t
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Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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7 CACTAC 3

Oy 1 CACTAC 5
Db 2 CACTAC 6

RESULT 8
LOCUS AX104946 8 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1138 from Patent WO0122972.
ACCESSION AX104946
VERSION AX104946.1 GI:13921143
KEYWORDS
SOURCE synthetic construct
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 8)
AUTHORS Kriegl, A.M., Schetter, C. and Vollmer, J.C.
TITLE DNA-based transposon system for the introduction of nucleic acid
JOURNAL Patent WO 0122972-A1 136 05-1998-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Source Location/Qualifiers
BASE COUNT 2 a 1 c 2 g 3 t
Query Match 100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 CACTAC 5
Db 2 CACTAC 6

RESULT 9
LOCUS AX268753 9 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0174342.
ACCESSION AX268753
VERSION AX268753.1 GI:16541825
KEYWORDS
SOURCE synthetic construct
ORGANISM
REFERENCE 1 (bases 1 to 9)
AUTHORS Gluchrest, B.A., Yaer, M. and Eller, M.
TITLE Use of locally applied DNA fragments
JOURNAL Patent WO 0174342-A1 29-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES
Source Location/Qualifiers
BASE COUNT 3 a 0 c 4 g 2 t
Query Match 100.0%; Score 5; DB 6; Length 9;

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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CANTAC 5
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LOCUS AX667174 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 623 from Patent WO242459.
ACCESSION AX667174.1 GI:29291326
KEYWORDS
SOURCE synthetic construct
ORGANISM Homo sapiens
AUTHORS Liu, Q.
REFERENCE 1. Position dependent recognition of gnm nucleotide triplets by zinc
finger proteins.
JOURNAL Sangamo BioScience Inc. (US)
PATENT: NO 0242459-A 623 30-MAY-2002;
FEATURES
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1 CANTAC 5
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RESULT 11
LOCUS AX668771 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2220 from Patent WO242459.
ACCESSION AX668771.1 GI:29291746
KEYWORDS
SOURCE synthetic construct
ORGANISM Homo sapiens
AUTHORS Liu, Q.
REFERENCE 1. Position dependent recognition of gnm nucleotide triplets by zinc
finger proteins.
JOURNAL Sangamo BioScience Inc. (US)
PATENT: NO 0242459-A 2220 30-MAY-2002;
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DEFINITION Sequence 2256 from Patent WO242459.
ACCESSION AX66807.1 GI:29291782
KEYWORDS
SOURCE synthetic construct
ORGANISM Homo sapiens
AUTHORS Liu, Q.
REFERENCE 1. Position dependent recognition of gnm nucleotide triplets by zinc
finger proteins.
JOURNAL Sangamo BioScience Inc. (US)
PATENT: NO 0242459-A 2256 30-MAY-2002;
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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CANTAC 5
2 CANTAC 6

RESULT 13
LOCUS S50583 9 bp mRNA linear PRI 07-MAY-1993
DEFINITION type I procollagen (human, mRNA Mutant, 9 nt).
ACCESSION S50583.1 GI:233928
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 9)
1. Sauerbrey, A., Castellanos, C.D. and Beecher, D.J.
Sauerbrey, T., Fontana, J., Sauerbrey, C., and Glycine alpha 2-694 of
type I procollagen in lethal osteogenesis imperfecta. The
conformational strain on the triple helix introduced by a glycine
substitution causes a decrease in the stability of the triple helix
J. Biol. Chem. 266 (24), 15608-15613 (1991).
MEDLINE 91340689
PUBMED 1874719
REMARK entry INCB1 gibtag 50583 from the original journal article.
This sequence comes from Fig 5A.
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1..9 /db_xref="taxon:9606"
1..9 /note="type I procollagen"
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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
Query Length 100.0%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CANTAC 5
2 CANTAC 4

Db 8 CANTAC 4

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Best Local Similarity: 100.0%; Pred. No. 1e-07;
Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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DB 10 CATCH 6

Search completed: December 31, 2003, 17:09:47
Job Time: 460.316 sec

Qy 1 CATCH 5
DB 9 CATCH 5

RESULT 14
LOCUS 9 bp DNA linear PAT 12-APR-1994
DEFINITION type I procollagen (human, Genomic DNA, 9 nt).
ACCESSION S50585
VERSION S50585.1 GI:233929
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens (human)
Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 9)
Gunsberg, J.T., Westerhausen, A., Constantinou, C.D. and Prockop, D.J.
Proc Natl Acad Sci USA 91:1034-1038 (1994)
Type I procollagen in lethal osteogenesis imperfecta. The
conformational strain on the triple helix introduced by a glycine
substitution can be transmitted along the helix
J Biol Chem 269 (24), 15878-15813 (1994)
91340689
1874719
GenBank staff at the National Library of Medicine created this
entry (NCBI accession S50585) from the original journal article.
This sequence comes from Fig 5B.
Location/Qualifiers
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/gene="type I procollagen"
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Best Local Similarity 100.0%; Pred. No. 4.5e-09;
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DB 9 CATCH 5

RESULT 15
LOCUS 10 bp DNA linear PAT 12-APR-1994
DEFINITION oligonucleotide.
ACCESSION A18263
VERSION A18263.1 GI:512254
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial human.
1 (bases 1 to 10)
Della Valle, P., Callegaro, L. and Negro, A.
Proc Natl Acad Sci USA 91:1034-1038 (1994)
Genetic vectors for the nerve growth
factor expression in eukaryotic cells.
Patent: EP 0412510-A 12-JUN-1991;
FIDIA S.p.A.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BASE COUNT 3 a 1 c 3 g 3 t

Query Match 100.0%; Score 5; DB 6; Length 10;


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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: December 31, 2003, 11:36:21, Search time 144.494 Seconds
Title: US-09-540-843-6
Perfect score: 5
Sequence: 1 catc 5
Scoring table: ISBIRITY.MUC
Gapop 10.0, Capext 1.0

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Fred greater than the observed number of results. Printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 5 100.0 7 20 AA210694 Oligonucleotide se
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c 7 5 100.0 7 23 AA214911 Melanogaster asso
c 8 5 100.0 8 22 AA012259 Direct repeat sequ

a presenat regulat
GAS compenagen
Cyclin D transcrip
Oligonucleotide se
Human DNA PCR prim
Human DNA PCR prim
Zinc finger proteol
Zinc finger proteol
Zinc finger proteol
Donor oligomer wit
Merlin exon 14 spl
Human DNA PCR prim
Anticancer duplex
Primer E19 for V.d
(GC-DA)n. (GC-DA)n
Yeast tag for addi
Yeast tag for addi
Yeast tag for NORP
Primer used in RAP
p53 serial analysi
Chromophore contai
Human monocyte and
Human monocyte and
Oligonucleotide us
Oligonucleotide us
Mouse DNA adapter
Primer MRL1 for mo
Human monocyte gen
Human monocyte gen
Human macrophage 9
Human macrophage 9
Human macrophage 9
Human macrophage 9
Human macrophage 9
Human macrophage 9

p53 activity: UV mimetic; UV-irradiation; UV-induced dermatosis;
UV-induced dermatosis; UV-induced dermatosis; UV-induced dermatosis;
apoptotic dermatitis; allergic rhinitis; conjunctivitis; photogingiv;
skin cancer; se.
XX XX Synthetic.
XX XX
XX XX 13-OCT-1999.
XX XX 24-MAR-1999; 9908-0006758.
XX XX 24-MAR-1999; 98US-0048927.
XX XX (UYEO-) UNIV BOOTH.
XX XX Glichtrest BA, Year M, Eller M;
XX XX WPI; 1999-543520/46.

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AA014907;
 14-FEB-2002 (first entry)
 Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 tumor necrosis factor inhibitor; photoprotecting; hyperproliferative disease;
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 conjunctivitis; allergic rhinitis; vitiligo; se.
 Synthetic.
 WO200174342-A2.
 11-OCT-2001.
 30-MAR-2001; 2001WO-US10162.
 31-MAR-2000; 2000US-0540843.
 (UTBO-) UNIV BOSTON.
 Glitchrest BA, Year M, Eller M;
 WPI; 2001-626338/72.
 Inhibiting proliferation of epithelial cells, useful e.g. for treating
 carcinoma, using specific oligonucleotides that mimic the effects of
 ultra-violet light.
 Claim 1; Page 36; 7app: English.
 The invention describes inhibition of mammalian epithelial cell
 proliferation by treating cells with at least one oligonucleotide, or
 its fragment. The compounds, which have cytostatic, anti-allergic,
 anti-inflammatory, dermatological, ophthalmological, anti-psoriatic,
 immunosuppressive activities, function as 'ultra-violet mimics' to induce
 DNA repair processes (or a protective response to later exposure to
 radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 or tumor necrosis factor inhibitor. The compounds may be used in the
 pathway, resulting in transient arrest of cell growth, allowing more time
 for DNA repair to occur before cell division takes place. The method is
 useful for treating carcinoma, hyperproliferative states (e.g. psoriasis or precancerous conditions),
 reduce photodamage, oxidative stress or damage; prevent skin cancer; treat
 allergic rhinitis and inflammation (atopic or contact dermatitis), treat
 conjunctivitis, allergic rhinitis and inflammation (atopic or contact dermatitis),
 cells caused by radiation or chemicals; increase melanin production
 (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 sequence is melanogenesis associated oligonucleotide #3, a truncated
 oligonucleotide that contain non-hydrolyzable backbones are used to
 inhibit proliferation of epithelial cells that contain damaged DNA. Also
 oligonucleotides used to inhibit mammalian epithelial cell
 proliferation, described in the method of the invention.
 Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 7;
 Local Similarity 100.0%; From No. 576906;
 Matches 5; Conservative 0; Mismatched 0; Indels 0; Gaps 0;
 1 C/TAC 5
 6 C/TAC 2

AA014911;
 14-FEB-2002 (first entry)
 Melanogenesis associated oligonucleotide #7.
 Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis inducer;
 tumor necrosis factor inhibitor; photoprotecting; hyperproliferative disease;
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
 conjunctivitis; allergic rhinitis; vitiligo; se.
 Synthetic.
 WO200174342-A2.
 11-OCT-2001.
 30-MAR-2001; 2001WO-US10162.
 31-MAR-2000; 2000US-0540843.
 (UTBO-) UNIV BOSTON.
 Glitchrest BA, Year M, Eller M;
 WPI; 2001-626338/72.
 Inhibiting proliferation of epithelial cells, useful e.g. for treating
 carcinoma, using specific oligonucleotides that mimic the effects of
 ultra-violet light.
 Claim 1; Page 38; 7app: English.
 The invention describes inhibition of mammalian epithelial cell
 proliferation by treating cells with at least one oligonucleotide, or
 its fragment. The compounds, which have cytostatic, anti-allergic,
 anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
 immunosuppressive activities, function as 'ultra-violet mimics' to induce
 DNA repair processes (or a protective response to later exposure to
 radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
 or tumor necrosis factor inhibitor. Probably they mimic products of
 DNA damage, or processed DNA-damage intermediates, by inducing the p53
 pathway, resulting in transient arrest of cell growth, allowing more time
 for DNA repair to occur before cell division takes place. The method is
 especially used to treat carcinoma but may also be used to treat other
 hyperproliferative states (e.g. psoriasis or precancerous conditions);
 reduce photodamage, oxidative stress or damage; prevent skin cancer; treat
 allergic rhinitis and inflammation (atopic or contact dermatitis), treat
 conjunctivitis, allergic rhinitis and inflammation (atopic or contact dermatitis),
 cells caused by radiation or chemicals; increase melanin production
 (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
 inhibit apoptosis, in response to DNA damage, in epithelial cell. This
 sequence is melanogenesis associated oligonucleotide #7, one of the
 oligonucleotides used to inhibit mammalian epithelial cell
 proliferation, described in the method of the invention.
 Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 7;
 Local Similarity 100.0%; From No. 576906;
 Matches 5; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

XX Differential display method; leucine-rich motif; transmembrane protein;
 XX secreted protein; primer; PCR; 98; human.

XX Homo sapiens.

XX Synthetic.

XX WO200259259-A2.

XX 01-AUG-2002.

XX 23-JAN-2002; 2002MO-IL00071.

XX 23-JUN-2001; 2001US-463158P.

XX (UFEA-1) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Kreschner DH;

XX WPI: 2002-599769/64.

XX Differential display method for identifying secreted or transmembrane
 XX protein, comprises contacting a DNA with a first primer that hybridizes
 XX to a sequence coding for a leucine-rich motif and with a second
 XX oligonucleotide primer -
 XX Class 52; Page 17; 37pp; English.

XX The invention relates to a differential display comprising contacting
 XX a DNA with a first primer that hybridizes to an oligonucleotide sequence
 XX coding for a leucine-rich motif, and with a second oligonucleotide primer
 XX to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from
 XX a cell, contacting the mRNA with a first primer that hybridizes to an
 XX oligonucleotide sequence coding for a leucine-rich motif, and with a second
 XX oligonucleotide primer to form cDNA-hybrid molecules, amplifying the
 XX amplified products from each sample to identify distinctive amplified
 XX products coding for at least one secreted or transmembrane protein. The
 XX proteins which are important for cell processes and play an important
 XX role in determining its phenotype, and which act as mediators for the
 XX transfer of signals from external environment, into the cell itself, thus
 XX primers used in the differential display method of the invention.

XX Sequence 9 BP; 1 A; 0 C; 2 G; 2 T; 4 other;

XX Query Match 100.0%; Score 5; DB 24; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2.9e+08;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CATAAC 5

XX 9 CATAAC 5

XX RESULT IS

XX 100.000000

XX ID ABQ71504 standard; DNA; 9 BP.

XX AC ABQ71504;

XX DT 28-AUG-2002 (first entry)

XX XX zinc finger protein related oligonucleotide target SEQ ID NO:623.

XX DE zinc finger protein; ZFP; DNA binding target; zinc finger; 88.

XX XX Homo sapiens.

XX CO Synthetic.

XX XX WO200242459-A2.

XX

PD 30-MAY-2002.

XX 20-NOV-2001; 2001MO-US43438.

XX 20-NOV-2000; 2000US-0716637.

XX (SANG-1) SANGOMO BIOSCIENCES INC.

XX L4U Q;

XX WPI: 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
 XX gene function and for human therapeutic and plant engineering.
 XX PT comprises first, second and third zinc fingers, ordered from N- to
 XX C-terminus -
 XX Example 1; Page 45; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to
 XX a target site, comprising F1, F2, F3 from N-terminus to C-terminus, where the
 XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 XX a third (S3) and a fourth (S4) subsequence, each subsequence comprising
 XX (1) a zinc finger subsequence, (2) a polynucleotide (111) encoding (I) or (II), and
 XX (3) designing (M) (I) involves selecting the F1 zinc finger such that
 XX it binds to the S1 target subsequence, selecting the F2 zinc finger such
 XX that it binds to the S2 target subsequence, selecting the F3 zinc finger
 XX such that it binds to the S3 target subsequence, thus designing (I)
 XX that binds to a target site. (I) is useful for recognition of triplet
 XX target subsequence having the nucleotide G in the 5'-most position of the
 XX target subsequence, and for recognition of triplet target subsequence
 XX therapeutics and plant engineering. (I), (II) or (III) is useful in
 XX a subject, diagnostic methods for sequence specific detection of
 XX a phenotype and function of gene expression. (I) has improved affinity
 XX and specificity for their target sequences, as well as enhanced
 XX stability. (I) is useful for recognition of triplet target subsequence
 XX represent DNA target sequences and zinc finger peptides which are given
 XX in the exemplification of the present invention.

XX Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 other;

XX Query Match 100.0%; Score 5; DB 24; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2.9e+08;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 0Y 1 CATAAC 5

XX 2 CATAAC 6

XX Search completed, December 31, 2003, 15:08:15

XX Job time : 145.494 secs

Copied from 09980559 on 05/19/2004

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RESULT 4
A1721735      16 bp      mRNA      linear      EST 07-JUN-2001
LOCUS       A1721735.1 GI:5040564
DEFINITION  Dario terio (zebrafish)
ACCESSION   A1721735.1
VERSION     A1721735.1
KEYWORDS    EST
SOURCE      Dario terio (zebrafish)
ORGANISM   Danio rerio (zebrafish)

Query Match
Best Local Similarity 100.0%; Score 5; DB 9; Length 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CNTAC 5
DB 9 CNTAC 13

RESULT 5
B0928185      16 bp      mRNA      linear      EST 06-NOV-2001
LOCUS       B0928185.1 GI:14322708
DEFINITION  Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes
; Cyprinidae; Dario.
ACCESSION   B0928185.1
VERSION     B0928185.1
KEYWORDS    EST, sapiens (human)
SOURCE      Homo sapiens
ORGANISM   Homo sapiens

Query Match
Best Local Similarity 100.0%; Score 5; DB 9; Length 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CNTAC 5
DB 9 CNTAC 13

RESULT 6
B0929050      17 bp      mRNA      linear      EST 06-NOV-2001
LOCUS       B0929050.1 GI:14323583
DEFINITION  HNC11-1-08 R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
ACCESSION   B0929050.1
VERSION     B0929050.1
KEYWORDS    EST
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens

Query Match
Best Local Similarity 100.0%; Score 5; DB 12; Length 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CNTAC 5
DB 8 CNTAC 12

FEATURES             Location/Qualifiers
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                        /db_xref="taxon:9606"
                        /tissue_type="Cartilage"
                        /lab_host="E.coli DH10 B"
                        /clone_lib="HNC (Human Normal Cartilage)"
                        /vector="pSPORT 1, Site_1, SalI, Site_2, NotI,
                        /directional="true"
BASE COUNT           4 a 6 c 2 g 3 t 1 others

Query Match
Best Local Similarity 100.0%; Score 5; DB 12; Length 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CNTAC 5
DB 8 CNTAC 12

FEATURES             Location/Qualifiers
     source            /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /tissue_type="Cartilage"
                        /lab_host="E.coli DH10 B"
                        /clone_lib="HNC (Human Normal Cartilage)"
                        /vector="pSPORT 1, Site_1, SalI, Site_2, NotI,
                        /directional="true"
BASE COUNT           4 a 6 c 2 g 3 t 1 others

TITLE
JOURNAL
AUTHORS
COMMENT

```

```

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 17)
AUTHORS
Kumar,S., Connor J.R., Dadds A.A., Halsey, M., Van Horn, M., Mao J.,
Sathyanarayanan, V., Agrawal, P., Badger, A.M., Lee, J.C., Gower, M. and
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
Osteoarthritis. Cartill. 9 (7), 641-653 (2001)
JOURNAL
MEDLINE
11597177
COMMENT
UNP0199: Sanjay Kumar
709 Swedenland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Fax: 610-270-5598
Email: sanjay.kumar@leqak.com
Seq primer: 7710m/Qualifiers
SOURCE
1. 17
/organism="Homo sapiens"
/ab_type="cDNA"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/notes="Vector: pGEMT 1, Site 1; SalI; Site 2; NotI;
Directional."
BASE COUNT
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ORIGIN
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Best Local Similarity 100.0% Pred. No. 1.8e+06; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
1 CATTAC 5
6 CATTAC 10
RESULTS
C21103 17 bp mRNA linear EST 06-DEC-2002
DEFINITION
Homo sapiens (human)
ACCESSION
C21103.1 GI:26125266
KEYWORDS
Unpublished
JOURNAL
COMMENT
Contact: Okubo, K.
Institute for Molecular and Cellular Biol.
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(x.3315)
Fax: 06-877-5111(x.3315)
E-mail: okubo@mol.f.uoi.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
sequence in this library and as well as in other 3-directed
sequences of the library and as well as in other 3-directed
sequences of the clones represented by this GS sequences is also
found there.
FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/ab_xref="taxon:9606"
/clone_id="Human adult (K.Okubo)"
/notes="One or more human adult tissue"
BASE COUNT
5 a 8 c 2 g 2 t
ORIGIN
Query Match 100.0% Score 5; DB 14; Length 17;
Best Local Similarity 100.0% Pred. No. 1.8e+06;

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Db          18 C2ATC 14

RESULT 14
A2341860/c 19 bp DNA linear GSS 29-SEP-2000
LOCUS      Mouse 10kb plasmid UUCGCM library mus musculus genomic
DEFINITION Clone UUCGCM074004 R, genomic survey sequence.
ACCESSION  GSS241860.1 GI:10419570
KEYWORDS   Mus musculus (mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 19)
AUTHORS    Dunn,D., Ayagi,A., Barber,M., Becom,T., Duval,B., Hamil,C.,
            M. Rose,M., Rose,R., Sches,R., Tingey,A., von Niederhausen,A.
            and Wright,D., Weis,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            Unpublished
JOURNAL    Unpublished
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 5696
            Email: daumgenetics@utah.edu
            Insert Length: 10000 Std Error: 0.00
            States: 077 CACAGCGAAGCCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
            1. 10000/Qualifiers
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /clone="UUCGCM074004"
            /vec_name="E. Coli strain XL10-Gold, TI-resistant, F-"/
            /clone_lib="Mouse 10kb plasmid UUCGCM library"
            /note="Vector: PM42nv; Purified genomic DNA from M.
            musculus C787/67 (male) was obtained from the Jackson
            Laboratory Mouse DNA Resources
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            20-gauge needle in a constant water bath. The sheared DNA
            was blunt ended with T4 DNA polymerase and ligated with
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            ligated DNA was size selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD22 (GI1472141GB/AP29072.1), a copy-number ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, sheared and transformed into
            electrocompetent cells (Stratagene) cells
            and selected for ampicillin resistance."
            BASE COUNT      4 a 4 c 6 g 5 t
            ORIGIN
            100 04; Score 5; DB 28; Length 19;
            Query Match      100 04; Pred. No. 1.9e+06;
            Best Local Similarity      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A2341860/c 19 bp DNA linear GSS 29-SEP-2000
LOCUS      Mouse 10kb plasmid UUCGCM library mus musculus genomic
DEFINITION Clone UUCGCM080016 R, genomic survey sequence.
ACCESSION  GSS241860.1 GI:10425086
KEYWORDS   Mus musculus (mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 19)
AUTHORS    Dunn,D., Ayagi,A., Barber,M., Becom,T., Duval,B., Hamil,C.,
            M. Rose,M., Rose,R., Sches,R., Tingey,A., von Niederhausen,A.
            and Wright,D., Weis,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            Unpublished
JOURNAL    Unpublished
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 5696
            Email: daumgenetics@utah.edu
            Insert Length: 10000 Std Error: 0.00
            States: 077 CACAGCGAAGCCTATGACC
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            1. 10000/Qualifiers
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            /mol_type="genomic DNA"
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            /clone="UUCGCM080016"
            /vec_name="E. Coli strain XL10-Gold, TI-resistant, F-"/
            /clone_lib="Mouse 10kb plasmid UUCGCM library"
            /note="Vector: PM42nv; Purified genomic DNA from M.
            musculus C787/67 (male) was obtained from the Jackson
            Laboratory Mouse DNA Resources
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            20-gauge needle in a constant water bath. The sheared DNA
            was blunt ended with T4 DNA polymerase and ligated with
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            ligated DNA was size selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD22 (GI1472141GB/AP29072.1), a copy-number ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, sheared and transformed into
            electrocompetent cells (Stratagene) cells
            and selected for ampicillin resistance."
            BASE COUNT      9 a 4 c 0 g 6 t
            ORIGIN
            100 04; Score 5; DB 28; Length 19;
            Query Match      100 04; Pred. No. 1.9e+06;
            Best Local Similarity      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CXTAC 5
DB 1 CXTAC 5

Search completed: December 31, 2003, 19:41:24
Job time : 574.494 secs

GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05, Search time 18.1304 Seconds
113,581 Million cell updates/sec

Title: US-09-540-843-6

Sequence: 1 catcac 5

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 226591565 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1. Issued Patents NA.../na/5A COMB seq.*
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3. /cm2.6/prodata//na/6A COMB seq.*
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Feed No. is the number of results predicted by chance to have a score as high as the best score found.
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	5	100.0	3	Sequence 20, Appl
C 3	5	100.0	5	Sequence 20, Appl
C 4	5	100.0	5	Sequence 20, Appl
C 5	5	100.0	7	US-08-615-170-12
C 6	5	100.0	7	US-09-048-927-3
C 7	5	100.0	3	Sequence 12, Appl
C 8	5	100.0	8	US-09-582-592-11
C 9	5	100.0	3	US-08-646-789A-8
C 10	5	100.0	9	US-08-646-789A-80
C 11	5	100.0	4	Sequence 27, Appl
C 12	5	100.0	4	US-09-319-224-08
C 13	5	100.0	10	US-08-335-565A-27
C 14	5	100.0	10	US-08-250-951-1
C 15	5	100.0	10	US-08-322-177A-422
C 16	5	100.0	10	US-08-351-748-23
C 17	5	100.0	10	US-08-351-748-25
C 18	5	100.0	10	US-08-351-748-25
C 19	5	100.0	10	US-08-351-748-25
C 20	5	100.0	10	US-08-430-536A-25
C 21	5	100.0	10	US-08-430-536A-25
C 22	5	100.0	10	US-08-171-718-45
C 23	5	100.0	10	US-08-684-547-23
C 24	5	100.0	10	US-08-684-547-23
C 25	5	100.0	10	US-08-684-547-25
C 26	5	100.0	10	US-08-469-318-174
C 27	5	100.0	10	US-08-468-609A-174

C 28 5 100.0 10 3 US-08-478-087-45
Sequence 24, Appl
C 30 5 100.0 10 3 US-09-063-450-24
Sequence 31, Appl
C 31 5 100.0 10 3 US-09-063-450-33
Sequence 1, Appl
C 32 5 100.0 10 3 US-09-123-438-1
Sequence 31, Appl
C 33 5 100.0 10 3 US-08-875-133-31
Sequence 174, Appl
C 34 5 100.0 10 4 US-08-446-872A-174
Sequence 1, Appl
C 35 5 100.0 10 4 US-09-724-7331-174
Sequence 23, Appl
C 36 5 100.0 10 4 US-09-475-447A-23
Sequence 34, Appl
C 37 5 100.0 10 4 US-09-427-844A-34
Sequence 34, Appl
C 38 5 100.0 10 4 US-08-408-833B-252
Sequence 265, Appl
C 39 5 100.0 10 4 US-09-508-753B-265
Sequence 273, Appl
C 40 5 100.0 10 4 US-09-508-753B-273
Sequence 284, Appl
C 41 5 100.0 10 4 US-09-508-753B-284
Sequence 103, Appl
C 42 5 100.0 10 4 US-09-508-753B-303
Sequence 103, Appl
C 43 5 100.0 10 4 US-09-508-753B-303
Sequence 103, Appl
C 44 5 100.0 10 4 US-09-508-753B-303
Sequence 103, Appl
C 45 5 100.0 10 4 US-09-508-753B-303
Sequence 103, Appl

ALIGNMENTS

RESULT 1
US-08-855-3728-20/c
Sequence 20, Application US/08853728

Patent No. 6,854,949
GENERAL INFORMATION:

APPLICANT: Mirzabekov, Andrei D

APPLICANT: Parinov, Sergei V

APPLICANT: Kirillov, Eugene V

APPLICANT: Kirillov, Eugene V

APPLICANT: Kirillov, Eugene V

TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic

INVENTOR: Chersakov, Michael J

CORRESPONDENCE ADDRESS:

ADDRESSER: CHERSAKOV & FLAYNIK

STREET: 20 N. Wacker Drive

CITY: Chicago, IL 60606

STATE: Illinois

COUNTRY: United States

ZIP: 60606

COMBID: 08853728

COMBID TYPE: 3.50 inch, 1.4 MB storage

COMPUTER: PC

SOFTWARE SYSTEM: Microsoft Windows 98

SOFTWARE: Microsoft Windows 98

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08853728

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/587,332

FILING DATE: 16-JAN-96

ATTORNEY: Chersakov, Michael J

REGISTRATION NUMBER: 33,664

REFERENCE/DOCCT NUMBER: RU-IN-95-027

TELEPHONE: (312) 621-1330

TELEFAX: (312) 621-0088

INSTRUMENTATION: ID NO. 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 bases

TYPE: nucleic acid

REFERENCE NO. 6090549 Applicable

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: yes

US-08-855-3728-20

Query Match

Best Local Similarity 100.0%; Score 5; DB 3; Length 5;

Seq. Local Similarity 100.0%; Prad. NO. 8.2e+07;

Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CINTAC 5
 DB 5 CINTAC 1

RESULT 2
 US-09-048-927-4/C
 FILE REFERENCE: B094-66A2 US/09/048/927
 GENERAL INFORMATION:
 APPLICANT: Glitchrest, Barbara A.
 APPLICANT: Elter, Mark
 TITLE OF INVENTION: Use of Locally Applied DNA Fragments
 CURRENT FILING DATE: 1998-03-26 US/09/048/927
 EARLIER APPLICATION NUMBER: 08/552,697
 EARLIER FILING DATE: 1996-06-03
 EARLIER PUBLICATION NUMBER: 1996-06-03
 EARLIER FILING DATE: 1995-06-06
 NUMBER OF SEQ ID NOS: 4
 SEQ ID NO 4: seqseq for Windows Version 3.0
 LENGTH: 5
 TYPE: DNA
 FEATURE:
 OTHER INFORMATION: Artificial Sequence
 OTHER INFORMATION: DNA Fragment
 09-048-927-4
 Query Match 100.0%; Score 5; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred No. 8.2e+07;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

1 CINTAC 5
 5 CINTAC 1

RESULT 3
 US-09-540-843-6/C
 FILE REFERENCE: B094-66A2 US/09/048/927
 GENERAL INFORMATION:
 APPLICANT: Glitchrest, Barbara A.
 APPLICANT: Elter, Mark
 TITLE OF INVENTION: Use of Locally Applied DNA Fragments
 CURRENT FILING DATE: 1998-03-26 US/09/048/927
 EARLIER APPLICATION NUMBER: 08/552,697
 EARLIER FILING DATE: 1996-06-03
 EARLIER PUBLICATION NUMBER: 1996-06-03
 EARLIER FILING DATE: 1995-06-06
 NUMBER OF SEQ ID NOS: 4
 SEQ ID NO 4: seqseq for Windows Version 3.0
 LENGTH: 5
 TYPE: DNA
 FEATURE:
 OTHER INFORMATION: Artificial Sequence
 OTHER INFORMATION: DNA Fragment
 09-048-927-4
 Query Match 100.0%; Score 5; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred No. 8.2e+07;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 1 CINTAC 5
 DB 5 CINTAC 1

RESULT 4
 US-08-615-170-10
 Sequence 10, Application US/08615170
 Patent No. 5787776
 GENERAL INFORMATION:
 APPLICANT: ORGANEL, Charles P.
 APPLICANT: AZARIE, Anthony
 APPLICANT: KANAKANN, M.
 APPLICANT: PABLANCO, Luis K.G.
 APPLICANT: HALL, Deborah E.
 APPLICANT: STEWART, Alexandre F.R.
 APPLICANT: STEWART, David
 TITLE OF INVENTION: Sequencing of
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 STREET: Stearns Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 FILE TYPE: COPY disk
 COMPILER: IBM
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT INVENTION DATA:
 APPLICATION NUMBER: US/08/615,170
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/01526
 FILING DATE: 06-FEB-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/191,493
 FILING DATE: 04-FEB-1994
 CLASSIFICATION: 435
 ATTORNEY INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 TELEPHONE: (415) 326-2400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2422
 INFORMATION FOR SEQ ID NO. 10:

Query Match 100.0%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels

1 CATAC 5
|||||
1 CATAC 5

RESULT 6
US-09-048-927-3/c
Sequence 3, Application US/09048927

;; GENERAL INFORMATION:
;; APPLICANT: Gilcrest, Barbara A.
;; APPLICANT: Yaar, Mina
;; APPLICANT: Yilgar, M...

```

; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927

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EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3

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// TYPE: DNA
// ORGANISM: Artificial Sequence
// FEATURE:

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US-09-048-927-3

Query Match	100.0%
Best Local Similarity	100.0%

Matches 5; Conservative 0;

10

6 CATAC 2

RESULT 7

03-09-142-393-11
; Sequence 11, Applic

GENERAL INFORMATION.

TITLE OF INVENTION

NUMBER OF SEQUENCES
CORRESPONDENCE A

ADDRESS: MU
STREET: 119 N

CITY: MINNEAPOLIS
STATE: MINNESOTA

ZIP: 55402

MEDIUM TYPE: COMPTON. TBM

OPERATING SYST: Pat

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1 APPLICATION NUMBER: 07/887,712
2 FILING DATE: 22-MAY-1992
3 INFORMATION FOR SEQ ID NO: 1:
4     SEQUENCE TYPE: nucleic acid
5     LENGTH: 9 bases
6     TYPE: nucleic acid
7     STRANDEDNESS: singular
8     TOPOLOGY: linear
9     MOLECULE TYPE: genomic DNA
10    DESCRIPTION: Genomic DNA
11    US-08-593-276-1
12
13    Query Match      100.0%; Score 5; DB 2; Length 9;
14    Best Local Similarity 100.0%; Fred. No. 4.5e+07;
15    Matches 5; Conservative 0; Mismatch 0; Indels
16
17    Oy      1 CAYAC 5
18    Db      8 CNAAC 4
19
20    RESULT 9
21    Sequence 8; Application US/08646789A
22    Patent No. 602863
23    GENERAL INFORMATION: John A.
24    NUMBER OF INVENTION: REGULATION OF GENE EXPRESSION
25    NUMBER OF SEQUENCES: 101
26    CORRESPONDING SEQUENCES:
27    CONCORDANCE POINTS: EDWARDS
28    STREET: 1155 Avenue of the Americas
29    CITY: New York
30    STATE: New York
31    COUNTRY: U. S. A.
32    ZIP: 10036-2711
33
34    COMPUTER READABLE FORM:
35    COMPUTER FILE:
36    COMPUTER SYSTEM: IBM PC compatible
37    OPERATING SYSTEM: PC-DOS/MS-DOS
38    SOFTWARE: Patent In Release #1.0, Version #1.30
39    APPLICATION NUMBER: US/08/646,789A
40    FILING DATE: May 24, 1996
41    CLASSIFICATION:
42    AT:
43    NAME: MicroSoft, S. Leslie
44    REGISTRATION NUMBER: 48,872
45    TELEPHONE: (212) 869-9523-006
46    TELECOMMUNICATION INFORMATION:
47    TELEPHONE: (212) 790-9090
48    TELEFAX: (212) 869-9741/8864
49    SEQUENCE CHARACTERISTICS:
50    INFORMATION FOR SEQ ID NO: 8:
51    LENGTH: 9 base pairs
52    STRANDEDNESS: singular
53    TOPOLOGY: linear
54    MOLECULE TYPE: DNA
55    US-08-646-789A-8
56
57    Query Match      100.0%; Score 5; DB 3; Length 9;
58    Best Local Similarity 100.0%; Fred. No. 4.5e+07;
59    Matches 5; Conservative 0; Mismatch 0; Indels
60
61    Oy      1 CAYAC 5
62    Db      5 CNAAC 1
63
64    RESULT 10
65    Sequence 8; Application US-08-646-789A-8/C
66    Patent No. 602863
67    GENERAL INFORMATION: John A.
68    NUMBER OF INVENTION: REGULATION OF GENE EXPRESSION
69    NUMBER OF SEQUENCES: 101
70    CORRESPONDING SEQUENCES:
71    CONCORDANCE POINTS: EDWARDS
72    STREET: 1155 Avenue of the Americas
73    CITY: New York
74    STATE: New York
75    COUNTRY: U. S. A.
76    ZIP: 10036-2711
77
78    COMPUTER READABLE FORM:
79    COMPUTER FILE:
80    COMPUTER SYSTEM: IBM PC compatible
81    OPERATING SYSTEM: PC-DOS/MS-DOS
82    SOFTWARE: Patent In Release #1.0, Version #1.30
83    APPLICATION NUMBER: US/08/646,789A
84    FILING DATE: May 24, 1996
85    CLASSIFICATION:
86    AT:
87    NAME: MicroSoft, S. Leslie
88    REGISTRATION NUMBER: 48,872
89    TELEPHONE: (212) 869-9523-006
90    TELECOMMUNICATION INFORMATION:
91    TELEPHONE: (212) 790-9090
92    TELEFAX: (212) 869-9741/8864
93    SEQUENCE CHARACTERISTICS:
94    INFORMATION FOR SEQ ID NO: 8:
95    LENGTH: 9 base pairs
96    STRANDEDNESS: singular
97    TOPOLOGY: linear
98    MOLECULE TYPE: DNA
99    US-08-646-789A-8
100
101    Query Match      100.0%; Score 5; DB 3; Length 9;
102    Best Local Similarity 100.0%; Fred. No. 4.5e+07;
103    Matches 5; Conservative 0; Mismatch 0; Indels
104
105    Oy      1 CAYAC 5
106    Db      5 CNAAC 1
107
108    RESULT 10
109    Sequence 8; Application US-08-646-789A-8/C
110    Patent No. 602863
111    GENERAL INFORMATION: John A.
112    NUMBER OF INVENTION: REGULATION OF GENE EXPRESSION
113    NUMBER OF SEQUENCES: 101
114    CORRESPONDING SEQUENCES:
115    CONCORDANCE POINTS: EDWARDS
116    STREET: 1155 Avenue of the Americas
117    CITY: New York
118    STATE: New York
119    COUNTRY: U. S. A.
120    ZIP: 10036-2711
121
122    COMPUTER READABLE FORM:
123    COMPUTER FILE:
124    COMPUTER SYSTEM: IBM PC compatible
125    OPERATING SYSTEM: PC-DOS/MS-DOS
126    SOFTWARE: Patent In Release #1.0, Version #1.30
127    APPLICATION NUMBER: US/08/646,789A
128    FILING DATE: May 24, 1996
129    CLASSIFICATION:
130    AT:
131    NAME: MicroSoft, S. Leslie
132    REGISTRATION NUMBER: 48,872
133    TELEPHONE: (212) 869-9523-006
134    TELECOMMUNICATION INFORMATION:
135    TELEPHONE: (212) 790-9090
136    TELEFAX: (212) 869-9741/8864
137    SEQUENCE CHARACTERISTICS:
138    INFORMATION FOR SEQ ID NO: 8:
139    LENGTH: 9 base pairs
140    STRANDEDNESS: singular
141    TOPOLOGY: linear
142    MOLECULE TYPE: DNA
143    US-08-646-789A-8

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; Sequence 80, Application US/08646789A
; Patent No. 6022663
; GENERAL INFORMATION:
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESS: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; FILE TYPE: IBM PC floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/646,789A
; FILING DATE: May 21, 1996
; CLASSIFICATION: 8007
; INVENTOR:
; NAME: Mierock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFO: 6541 PENNIS
; LENGTH: 9 base pairs
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRATEGY: single
; MOLECULE TYPE: linear
; TOPOLGY: linear
; SEQ ID NO 1
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; Query Match 100.0%; Score 5; DB 3; Length 9;
; Best Local Similarity 100.0%; Pred. No. 4.5e+07;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 1 CNTAC 5
; 5 CNTAC 1
;
; RESULT 11
; US-09-544-927-1/c
; Sequence 1, Application US/0948927
; Patent No. 6157056
; GENERAL INFORMATION:
; TITLE OF INVENTION: Locally Applied DNA Fragments
; APPLICANT: Glaxo, Barbara A.
; APPLICANT: Year, Mina
; APPLICANT: Elter, Mark
; FILE REFERENCE: B99A-88A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
; US-09-540-927-1
;
; Query Match 100.0%; Score 5; DB 3; Length 9;
; Best Local Similarity 100.0%; Pred. No. 4.5e+07;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 1 CNTAC 5
; 5 CNTAC 1
;
; RESULT 12
; US-09-546-68
; Sequence 68, Application US/09319648
; Patent No. 6451530
; GENERAL INFORMATION:
; TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
; FORMATION for Detection of Nucleic Acid Hybridization
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; FILE TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; APPLICATION NUMBER: US/09/319,648
; FILING DATE: 30-Jul-1999
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,844
; FILING DATE: 13-DEC-1996
; REFERENCE/DOCKET NUMBER: US97/22448
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 48,631
; REFERENCE/DOCKET NUMBER: 015280-288100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 767-0300
; TELEFAX: (415) 767-0300
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRATEGY: single
; MOLECULE TYPE: linear
; TOPOLGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
;
; US-09-319-648-68
;
; Query Match 100.0%; Score 5; DB 4; Length 9;
; Best Local Similarity 100.0%; Pred. No. 4.5e+07;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 1 CNTAC 5
; 3 CNTAC 7
;
; RESULT 13
; US-08-335-565A-27/c
; Sequence 27, Application US/0833565A
; Patent No. 6525711
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; APPLICANT: L.A. Kening
; OTHER INFORMATION:
; APPLICANT: Rouse, Douglas I.

```

APPLICANT: GUNTER, Thomas E.
TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: 33

STREET: 1500 S. 15th Street, Suite 100
CITY: Madison

STATE: WI
COUNTRY: USA

ZIP: 53701-2113

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,565A

FILING DATE: 07/NOV-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Gunter

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296.93065

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE LENGTH: 10 base pair

TYPE: nucleic acid

STANDARDS: single

MOLECULE TYPE: DNA (genomic)

Query Match 100.0%; Score 5; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.6e+04;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATA 5

10 CATA 6

08-335-565A-27

US-08-250-951-1

GENERAL INFORMATION:
APPLICANT: Michael J. Heller

TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC

TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

STREET: 1256 High Bluff Drive, Suite 300

STATE: California

COUNTRY: USA

ZIP: 92130

COMPUTER: IBM PC compatible

OPERATING SYSTEM: SPARC/OS/2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/250,951

FILING DATE: 07/NOV-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/990,262

FILING DATE: 07-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas

REGISTRATION/DOCKET NUMBER: 34,163

REFERENCE/DOCKET NUMBER: HEL0002P

TELEPHONE: 619-792-3680

TELEFAX: 619-792-8477

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE LENGTH: 10 base pair

TYPE: nucleic acid

STANDARDS: single

MOLECULE TYPE: DNA (genomic)

FEATURES: NO

NAME/KEY: misc feature

LOCATION: 10

ATTORNEY/AGENT INFORMATION: /note: "Paper chromosome at the 3'

OTHER INFORMATION: T nucleotide"

US-08-250-951-1

Query Match 100.0%; Score 5; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.6e+04;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATA 5

4 CATA 8

US-08-232-233-1

GENERAL INFORMATION:
APPLICANT: Michael J. Heller

TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC

TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

STREET: 611 West Sixth Street

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,233

FILING DATE: May 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/790,262

FILING DATE: No. 565322ember 7, 1992

NAME: Murphy, David B.

REGISTRATION NUMBER: 31,125

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pair

TYPE: nucleic acid


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: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: IS_CIRCULAR: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: misc_feature
: QUALITY: 100.00
: OTHER INFORMATION: /note="Donor chromosome at the 3' T nucleotide"
US-09-232-233-1
Query Match 100.00; Score 5; Dg 1; Length 10;
Best Local Similarity 100.00; Pred. No. 8.68e-04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CATAC 5
4 CATAC 0

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Search completed: January 1, 2004, 00:32:18
Job time : 19.5415 secs

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GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00, Search time 58 9911 Seconds
(without alignment)
296.996 Million cell updates/sec

Title: US-09-540-843-6
Perfect score: 5
Sequences: 1 catc 5

Scoring table: IDENTITY, NUC

Gapop 10.0, Gapext 1.0

Searched: 246343 seqs, 170657950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing Match 10%

Listing first 4 summaries

Database:

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2. /cgn2_6/prodata/1/publna/US06_NEW_PUB.seq*
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18. /cgn2_6/prodata/1/publna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Length	DB ID	Description
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c	2	5	100.0	5	US-10-122-630-6	Sequence 6, Appl
c	3	5	100.0	5	US-10-122-631-6	Sequence 6, Appl
c	4	5	100.0	5	US-10-122-631-6	Sequence 6, Appl
c	5	5	100.0	7	US-10-027-632-178023	Sequence 178023,
c	6	5	100.0	7	US-10-027-632-178043	Sequence 178043,
c	7	5	100.0	7	US-10-027-632-178043	Sequence 178043,
c	8	5	100.0	7	US-10-122-630-3	Sequence 3, Appl
c	9	5	100.0	7	US-10-122-630-7	Sequence 7, Appl
c	10	5	100.0	7	US-10-122-630-7	Sequence 7, Appl
c	11	5	100.0	7	US-10-122-631-7	Sequence 7, Appl
c	12	5	100.0	7	US-10-122-631-7	Sequence 7, Appl
c	13	5	100.0	8	US-09-142-593-11	Sequence 11, Appl
c	14	5	100.0	8	US-09-927-886-17	Sequence 17, Appl
c	15	5	100.0	8	US-09-881-014-6	Sequence 6, Appl

c	16	5	100.0	8	US-10-122-630-24	Sequence 24, App
c	17	5	100.0	8	US-10-122-630-24	Sequence 24, App
c	18	5	100.0	8	US-10-122-630-24	Sequence 24, App
c	19	5	100.0	8	US-10-122-630-24	Sequence 24, App
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c	22	5	100.0	8	US-10-122-630-24	Sequence 24, App
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c	30	5	100.0	8	US-10-122-630-24	Sequence 24, App
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c	45	5	100.0	8	US-10-122-630-24	Sequence 24, App

ALIGNMENTS

RESULT 1
US-10-122-630-4/c
Sequence 4, Application US/10122630
GENERAL INFORMATION:
APPLICANT: Gluchrest, Barbara A.
APPLICANT: Yiller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
CURRENT FILING DATE: 2002-04-12, 630
CURRENT FILING DATE: 2002-04-12, 630
PRIOR APPLICATION NUMBER: US 09/467, 012
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048, 927
PRIOR APPLICATION NUMBER: US 09/540, 843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 5
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-4

Query Match 100.0%, Score 5, DB 15, Length 5,
Best Local 100.0%, Pred No. 6,7808;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CMTAC 5

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Db          |||||
           5 CATA 1

RESULT 2
US-10-122-630-6
; Sequence 6, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Glitchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yell, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054-1088-019
; CURRENT APPLICATION NUMBER: US/10/122,630
; PRIOR APPLICATION NUMBER: US 58/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/00386
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-6

Query Match      100.0%; Score 5; DB 15; Length 5;
Ref Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

           1 CATA 5
           5 CATA 5

RESULT 3
US-10-122-633-6
; Sequence 4, Application US/10122633
; Publication No. US2003003261A1
; GENERAL INFORMATION:
; APPLICANT: Glitchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yell, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054-1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR APPLICATION NUMBER: PCT/US96/00386
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

Query Match      100.0%; Score 5; DB 15; Length 5;
Ref Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

           1 CATA 5
           5 CATA 5

RESULT 4
US-10-122-633-6
; Sequence 6, Application US/10122633
; Publication No. US2003003261A1
; GENERAL INFORMATION:
; APPLICANT: Glitchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yell, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054-1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR APPLICATION NUMBER: PCT/US96/00386
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

Query Match      100.0%; Score 5; DB 15; Length 5;
Ref Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

           1 CATA 5
           5 CATA 5

RESULT 5
US-10-037-632-178029
; Sequence 178029, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: David G.
; APPLICANT: Yell, Mina
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 0054-1088-019
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/199,076
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-09-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178029

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; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029

Query Match
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 1 CATAC 5

RESULT 6
US-10-027-632-178043
Sequence 178043, Application US/10027632
Publication No. US20030204075A9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1998-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
LENGTH: 7
TYPE: DNA
ORGANISM: Human
US-10-027-632-178043

Query Match
Best Local Similarity 100.0%; Score 5; DB 13; Length 7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 1 CATAC 5

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Copied from 09980559 on 05/19/2004

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; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029

Query Match
Best Local Similarity 100.0%; Score 5; DB 14; Length 7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 1 CATAC 5

RESULT 8
US-10-027-632-178043
Sequence 178043, Application US/10027632
Publication No. US20030204075A9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1998-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
LENGTH: 7
TYPE: DNA
ORGANISM: Human
US-10-027-632-178043

Query Match
Best Local Similarity 100.0%; Score 5; DB 14; Length 7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 1 CATAC 5

RESULT 9
US-10-122-630-3/c
Sequence 3, Application US/10122630
Publication No. US20030303261U1
APPLICANT: Glitchrest, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Isaar, Mima

```

```

Db          6 CMTAC 2

RESULT 11
US-10-122-633-7/c
Sequence 3 Application US/10122633
Publication No. US20030032611A1
GENERAL INFORMATION:
APPLICANT: Glitchrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
Oligonucleotides
FILE REFERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US/10122-633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2001-03-30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 7
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match          100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CMTAC 5
6 CMTAC 2

US-10-122-630-3
US-10-122-630-7/c
Sequence 7 Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Glitchrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
Oligonucleotides
FILE REFERENCE: 0054-1088-018
CURRENT APPLICATION NUMBER: US/10122-630
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2001-03-30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-631-7
US-10-122-631-7/c
Sequence 7 Application US/10122631
Publication No. US20030032611A1
GENERAL INFORMATION:
APPLICANT: Glitchrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
Oligonucleotides
FILE REFERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US/10122-633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2001-03-30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match          100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CMTAC 5
6 CMTAC 2

US-10-122-633-7/c
Sequence 7 Application US/10122633
Publication No. US20030032611A1
GENERAL INFORMATION:
APPLICANT: Glitchrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
Oligonucleotides
FILE REFERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US/10122-633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2001-03-30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match          100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CMTAC 5
6 CMTAC 2

US-10-122-633-7/c
Sequence 7 Application US/10122633
Publication No. US20030032611A1
GENERAL INFORMATION:
APPLICANT: Glitchrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
Oligonucleotides
FILE REFERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US/10122-633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2001-03-30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match          100.0% Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CMTAC 5
6 CMTAC 2

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RESULT 13 -593-11
; Sequence 11, Application US/09142593
; Patent No. US20020016975A1
; GENERAL INFORMATION:
; APPLICANT: ET AL.
; TITLE OF INVENTION: DNA-BASED TRANSPORT SYSTEM FOR THE
; INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL.
; CORRESPONDENCE:
; ADDRESSER: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55402
; COMMERCIAL FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; APPLICATION NUMBER: US/09/142,593
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 60/040,664
; FILING DATE: 11-MAR-1997
; PRIOR APPLICATION NUMBER: 60/053,868
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION NUMBER: 60/065,303
; FILING DATE: 11-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CT/US98/04687
; FILING DATE: 11-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SNOBERG, VICTORIA A.
; ADDRESS: 1000 PARK AVENUE, SUITE 1700
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; TELEPHONE: 612-305-1226
; REFERENCE/DOCKET NUMBER: 110-00450101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: double strand
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-142-593-11
; Query Match 100.0%; Score 5; DB 9; Length 8;
; Best Local Similarity 100.0%; Pred. No. 4.2e+08;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTAC 5
Db 2 CATTAC 6

; Sequence 17, Application US/0927886
; Patent No. US20020115216A1
; GENERAL INFORMATION:
; APPLICANT: Kren, Cheryl
; TITLE OF INVENTION: Composition for Delivery of Compounds to Cells
; CORRESPONDENCE:
; ADDRESSER: Hackett, Perry
; STREET: 1000 PARK AVENUE, SUITE 1700
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; TELEPHONE: 612-305-1226
; REFERENCE/DOCKET NUMBER: 110-00450101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: DNA
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Artificial Sequence
; OTHER INFORMATION: Direct repeat sequence
US-09-861-014-6
; Query Match 100.0%; Score 5; DB 10; Length 8;
; Best Local Similarity 100.0%; Pred. No. 4.2e+08;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTAC 5
Db 2 CATTAC 6

Search completed: January 1, 2004, 01:10:37
Job time : 38.2511 secs

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:

December 31, 2003, 11:36:21 ; Search time 644.443 Seconds
444.364 Million cell updates/sec
(without alignments)

Title: US-09-540-843-7

Perfect score: 7

Sequence: 1 agatgca 7

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 268871 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: gb-hg-hum*

2: gb-hg*

3: gb-in*

4: gb-om*

5: gb-pat*

6: gb-pl*

7: gb-ph*

8: gb-ro*

9: gb-sta*

10: gb-un*

11: gb-vi*

12: gb-w*

13: gb-z*

14: gb-ba*

15: es-ba*

16: es-in*

17: es-hum*

18: es-mu*

19: es-mu*

20: es-mu*

21: es-or*

22: es-pat*

23: es-pl*

24: es-ro*

25: es-sta*

26: es-to*

27: es-un*

28: es-vi*

29: es-w*

30: es-hg-hum*

31: es-hg-hum*

32: es-hg-Other*

33: es-hg-mus*

34: es-hg-pln*

35: es-hg-pln*

36: es-hg-mam*

37: es-hg-vrt*

38: es-hg-vrt*

39: es-hg-hum*

40: es-hgo-hum*

41: es-hgo-Other*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	6	AZ68755 Sequence
2	7	100.0	7	6	AZ68759 Sequence
3	7	100.0	9	6	AZ68753 Sequence
4	7	100.0	10	6	AZ68757 Sequence
5	7	100.0	10	6	AZ68758 Sequence
6	7	100.0	10	6	AZ68759 Sequence
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ALIGNMENTS

RESULT 1	AZ68755	AZ68755	7 bp	DNA
DEFINITION	AZ68755	3 From Patent WO0174312.		
ACCESSION	AZ68755	GI:16541827		
VERSION	AZ68755	1		
KEYWORDS		synthetic construct		
SOURCE		artificial sequences		
ORGANISM		Gilchrist, B.A., Year, M. and Eller, M.		
REFERENCE		Use of locally applied dna fragments		
AUTHORS		Patent: WO 017432-A3 11-OCT-2001,		
TITLE		INSTRUMENTS OF BOSTON UNIVERSITY (US)		
JOURNAL				

Linear PAT 29-OCT-2001


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Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATGCA 7
Db 1 AGATGCA 7

RESULT 10
LOCUS AX624159 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1200 from Patent WO02053774.
ACCESSION AX624159.1 GI:28452100
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
Peterson D., Conrad M. and Hofmann K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 1375 11-JUN-2002;
Hensel Kommandoegellechaft auf Aktien (DE)
FEATURES
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/db_xref=taxon:9606 3 t
BASE COUNT
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ORIGIN
Query Match
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Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATGCA 7
Db 5 AGATGCA 11

RESULT 11
LOCUS AX624134 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1375 from Patent WO02053774.
ACCESSION AX624134.1 GI:28452275
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
Peterson D., Conrad M. and Hofmann K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 1375 11-JUN-2002;
Hensel Kommandoegellechaft auf Aktien (DE)
FEATURES
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/mol_type="genomic DNA"
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BASE COUNT
4 a 2 c 2 g
ORIGIN

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Query Match
100.0%; Score 7; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATGCA 7
Db 1 AGATGCA 7

RESULT 12
LOCUS AX625574 2615 from Patent WO02053774.
ACCESSION AX625574.1 GI:28453515
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
Peterson D., Conrad M. and Hofmann K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 3223 11-JUN-2002;
Hensel Kommandoegellechaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref=taxon:9606 3 t
BASE COUNT
3 a 4 c 1 g
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Query Match
100.0%; Score 7; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATGCA 7
Db 9 AGATGCA 3

RESULT 13
LOCUS AX626182 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3223 from Patent WO02053774.
ACCESSION AX626182.1 GI:28454220
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
Peterson D., Conrad M. and Hofmann K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 3223 11-JUN-2002;
Hensel Kommandoegellechaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref=taxon:9606 2 t
BASE COUNT
5 a 0 c 4 g
ORIGIN
Query Match
100.0%; Score 7; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATGCA 7
Db 1 AGATGCA 7

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[illegible]


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1 STRANDEDNESS: single
2 TOPOLOGY: linear
3 MOLECULE TYPE: DNA (genomic)
4 PHYSICAL: NO
5 ANTI-SENSE: NO
6 FEATURE:
7 NAME/KEY: misc_feature
8 LOCATION: chr1:100000-100000
9 OTHER INFORMATION: /note="Donor chromosome at the 3' T nucleotide"
10 US-08-232-233-1
11
12 Query Match 100.0%; Score 5; DS 1; Length 10;
13 Best Local Similarity 100.0%; Pred. No. 8.6e-04;
14 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
15
16 1 GTATG 5
17      |||||
18 8 GTATG 4
19
20
21 Search completed: January 1, 2004, 00:32:18
22 Job time : 19.5415 secs
  
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GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05, Search time 27.2925 Seconds
113.581 Alignment cell updated/sec

us-09-540-843-3
Title: Perfect score: 7
Sequence: 1 agataga 7
Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

56978 seqs, 22651566 residues
Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing Minimum Match 0%
Minimum Match 0%
Listing first 45 summaries

Databases:
1: Issued_Patents.NA.*
2: /cgn2_e/prodata/1/in/5b_COMB.seq.*
3: /cgn2_e/prodata/1/in/6a_COMB.seq.*
4: /cgn2_e/prodata/1/in/6b_COMB.seq.*
5: /cgn2_e/prodata/1/in/6c_PCTUS_COMB.seq.*
6: /cgn2_e/prodata/1/in/backfiles.seq.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	3	US-09-048-927-3	Sequence 1, Appl
2	7	100.0	9	US-09-048-927-1	Sequence 3, Appl
3	7	100.0	13	US-09-048-927-1	Sequence 12, Appl
4	7	100.0	14	US-09-048-927-1	Sequence 27, Appl
5	7	100.0	14	US-08-485-133-27	Sequence 27, Appl
6	7	100.0	14	US-08-746-805A-4	Sequence 4, Appl
7	7	100.0	15	US-08-314-847-327	Sequence 327, Appl
8	7	100.0	15	US-08-314-847-327	Sequence 327, Appl
9	7	100.0	15	US-08-671-071B-2	Sequence 2, Appl
10	7	100.0	15	US-08-747-121-4	Sequence 4, Appl
11	7	100.0	15	US-08-747-121-4	Sequence 4, Appl
12	7	100.0	15	US-08-585-684B-1315	Sequence 1315, Appl
13	7	100.0	15	US-08-485-133-28	Sequence 28, Appl
14	7	100.0	15	US-09-004-714A-33	Sequence 33, Appl
15	7	100.0	15	US-09-004-714A-33	Sequence 33, Appl
16	7	100.0	15	US-09-048-927-3	Sequence 6, Appl
17	7	100.0	15	US-09-048-927-3	Sequence 7, Appl
18	7	100.0	15	US-09-048-927-3	Sequence 130, Appl
19	7	100.0	15	US-09-038-073-16	Sequence 16, Appl
20	7	100.0	15	US-08-932-140C-65	Sequence 6, Appl
21	7	100.0	15	US-08-932-140C-7	Sequence 7, Appl
22	7	100.0	15	US-08-932-140C-7	Sequence 55, Appl
23	7	100.0	16	US-07-971-28A-59	Sequence 24, Appl
24	7	100.0	16	US-08-719-591-24	Sequence 24, Appl
25	7	100.0	16	US-08-256-426B-59	Sequence 59, Appl
26	7	100.0	16	US-08-256-426B-59	Sequence 59, Appl
27	7	100.0	17	US-08-330-850-461	Sequence 461, Appl

ALIGNMENTS

RESULT 1

US-09-048-927-3

Sequence 3, Application US/09048927

GENERAL INFORMATION:

APPLICANT: GlaxoSmithKline

APPLICANT: Year, Mins

FILE REFERENCE: B094-68A2

CURRENT FILING DATE: 1998-06-03

EARLIER FILING DATE: 1998-06-03

EARLIER FILING DATE: 1998-06-03

EARLIER FILING DATE: 1998-06-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NOS:

LENGTH: 7

TYPE: DNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: DNA Fragment

US-09-048-927-3

Query Match 100.0% Score 7, DB 3, Length 7;

Best Local Similarity 100.0% Prod. No. 5 94:07

Matches 7; Conservative 0; Mismatch 0; Indels 0

Qy 1 AGATAGA 7

Db 1 AGATAGA 7

RESULT 2

US-09-048-927-1

Sequence 1, Application US/09048927

GENERAL INFORMATION:

APPLICANT: GlaxoSmithKline

APPLICANT: Year, Mins

FILE REFERENCE: B094-68A2

CURRENT FILING DATE: 1998-06-03

EARLIER FILING DATE: 1998-06-03

EARLIER FILING DATE: 1998-06-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NOS:

LENGTH: 7

TYPE: DNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: DNA Fragment

US-09-048-927-1

Query Match 100.0% Score 7, DB 3, Length 7;

Best Local Similarity 100.0% Prod. No. 5 94:07

Matches 7; Conservative 0; Mismatch 0; Indels 0

Qy 1 AGATAGA 7

Db 1 AGATAGA 7

Sequence 461, Appl


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1  TITLE OF INVENTION:  AND METHODS OF USE THEREOF
2  NUMBER OF SEQUENCES:  14
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Pennette & Edmunds
5  STREET:  1115 Avenue of the Americas
6  CITY:  New York
7  STATE:  NY
8  COUNTRY:  USA
9  ZIP:  10036-2711
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Diskette
12 OPERATING SYSTEM:  DOS
13 SOFTWARE:  FastSeq Version 2.0
14 CURRENT APPLICATION DATA:
15 FILING DATE:  08-NOV-1998
16 CLASSIFICATION:  536
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER:
19 FILING DATE:
20 ATTORNEY/AGENT INFORMATION:
21 NAME:  Raymond A. Pennette, Jr.
22 REGISTRATION NUMBER:  8511-009
23 REFERENCE/DOCKET NUMBER:  8511-009
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE:  (212) 699-9090
26 TELEFAX:  (212) 699-9084
27 INFORMATION FOR SEQ ID NO:  4:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH:  14 base pairs
30 TYPE:  nucleic acid
31 STRANDNESS:  single
32 FEATURE:
33 NAME/KEY:  Modified Base
34 LOCATION:  1
35 DESCRIPTION:  Where N is any nucleotide
36
37 Query Match 100.0%; Score 7; DB 2; Length 14;
38 Sequence 24,669,913; Pos 100.0%; Prod No. 8,680,3;
39 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
40
41 1 ACTATGA 7
42 14 ACTATGA 8
43
44 RESULT 7:
45 US-09-334-847-24
46 Sequence 24,669,913
47 Application US/08334847
48 GENERAL INFORMATION:
49 APPLICANT:  McSwiggen, James
50 APPLICANT:  Praper, Kenneth
51 APPLICANT:  Wolf, Tod
52 APPLICANT:  Wolf, Tod
53 TITLE OF INVENTION:  METHOD AND REAGENT FOR
54 IDENTIFYING AND PURIFYING SYNCTIAL VIRUS
55 TITLE OF INVENTION:  SYNCTIAL VIRUS
56 NUMBER OF SEQUENCES:  909
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE:  Pennette & Edmunds
59 STREET:  631 West Fifth Street
60 STREET:  Suite 4700
61 CITY:  Los Angeles
62 STATE:  California
63 COUNTRY:  U.S.A.
64 ZIP:  90071-2066
65 COMPUTER READABLE FORM:  Diskette, 1.44 Mb
66 MEDIUM TYPE:  storage
67 COMPUTER:  IBM Compatible
68 OPERATING SYSTEM:  IBM P.C. DOS 5.0
69 CURRENT APPLICATION DATA:
70 APPLICATION NUMBER:  US/08/334,847
71 FILING DATE:  No. 5693532ember 4, 1994
72 APPLICATION INFORMATION:
73 FILING DATE:
74 ATTORNEY/AGENT INFORMATION:
75 NAME:  Raymond A. Pennette, Jr.
76 REGISTRATION NUMBER:  32,327
77 REFERENCE/DOCKET NUMBER:  209/032
78 TELECOMMUNICATION INFORMATION:

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1  MEDIUM TYPE:  storage
2  COMPUTER:  IBM Compatible
3  OPERATING SYSTEM:  IBM P.C. DOS 5.0
4  SOFTWARE:  Word Perfect 5.1
5  CURRENT APPLICATION DATA:
6  APPLICATION NUMBER:  US/08/334,847
7  FILING DATE:  No. 5693532ember 4, 1994
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER:
10 FILING DATE:
11 ATTORNEY/AGENT INFORMATION:
12 NAME:  Raymond A. Pennette, Jr.
13 REGISTRATION NUMBER:  327
14 REFERENCE/DOCKET NUMBER:  209/032
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE:  (212) 490,1600
17 TELEFAX:  (212) 952-0448
18 INFORMATION FOR SEQ ID NO:  24:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH:  15 base pairs
21 TYPE:  nucleic acid
22 STRANDNESS:  single
23 FEATURE:
24 NAME/KEY:  Modified Base
25 LOCATION:  1
26 DESCRIPTION:  Where N is any nucleotide
27
28 Query Match 100.0%; Score 7; DB 1; Length 15;
29 Sequence 327,669,909; Pos 100.0%; Prod No. 8,680,3;
30 Best Local Similarity 100.0%; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
31
32 1 ACTATGA 7
33 5 AGAUGA 11
34
35 RESULT 8
36 US-09-334-847-327
37 Application US/08334847
38 GENERAL INFORMATION:
39 APPLICANT:  McSwiggen, James
40 APPLICANT:  Praper, Kenneth
41 APPLICANT:  Wolf, Tod
42 APPLICANT:  Wolf, Tod
43 TITLE OF INVENTION:  METHOD AND REAGENT FOR
44 IDENTIFYING AND PURIFYING SYNCTIAL VIRUS
45 TITLE OF INVENTION:  SYNCTIAL VIRUS
46 NUMBER OF SEQUENCES:  909
47 CORRESPONDENCE ADDRESS:
48 ADDRESSEE:  Pennette & Edmunds
49 STREET:  631 West Fifth Street
50 STREET:  Suite 4700
51 CITY:  Los Angeles
52 STATE:  California
53 COUNTRY:  U.S.A.
54 ZIP:  90071-2066
55 COMPUTER READABLE FORM:  Diskette, 1.44 Mb
56 MEDIUM TYPE:  storage
57 COMPUTER:  IBM Compatible
58 OPERATING SYSTEM:  IBM P.C. DOS 5.0
59 CURRENT APPLICATION DATA:
60 APPLICATION NUMBER:  US/08/334,847
61 FILING DATE:  No. 5693532ember 4, 1994
62 APPLICATION INFORMATION:
63 FILING DATE:
64 ATTORNEY/AGENT INFORMATION:
65 NAME:  Raymond A. Pennette, Jr.
66 REGISTRATION NUMBER:  32,327
67 REFERENCE/DOCKET NUMBER:  209/032
68 TELECOMMUNICATION INFORMATION:

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TELEPHONE: (213) 489-1600
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 327:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDNESS: single
US-08-334-847-327

Query Match 100.0% Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Prd. No. 8-6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
5 AGTATGA 11

RESULT 9
Sequence 2, Application US/08671071B
Prd. No. 8-6e+03
GENERAL INFORMATION:
APPLICANT: Grandgenett, Duane
TITLE OF INVENTION: An in vitro method for concerted integration of
sequences into a genome
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grandgenett, Duane
ADDRESS: 4610 Marietta Ave
CITY: Brentwood
STATE: Missouri
COUNTRY: USA
ZIP: 63104

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch;
OPERATING SYSTEM: IBM PC
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
FILING DATE: 06/27/96
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 577-8406
TELEFAX: (314) 577-8406
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDNESS: double
MOLUCULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE: DMS PLANT plasmid and pGEM plasmid.
IMMEDIATE SOURCE: Same as in 2.vi.
FEATURE:
OTHER INFORMATION: The sequence is the bottom strand of
OTHER INFORMATION: M2 US and the pGEM target of the top clone shown in
OTHER INFORMATION: Figure 14 of the original application.

Query Match 100.0% Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Prd. No. 8-6e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
9 AGTATGA 3

RESULT 10
US-08-747-121-4/c
Prd. No. 8-6e+03
GENERAL INFORMATION:
APPLICANT: Murphy, Gerald
ADDRESS: 15000 S. 1st Ave
CITY: Scottsdale, AZ
STATE: Arizona
COUNTRY: USA
ZIP: 85260
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM PC
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 08/08/97
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE: 08/08/97
FILING DATE: 08/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Saidwin, Geraldine G
REFERENCE/DOCKET NUMBER: 17,52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 868-9890
TELEFAX: (212) 868-9890
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDNESS: single
MOLUCULE TYPE: linear
FEATURE:
NAME/KEY: Modified Base
OTHER INFORMATION: Where N is any nucleotide
US-08-747-121-4

Query Match 100.0% Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Prd. No. 8-6e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGTATGA 7
DB 15 AGTATGA 9

RESULT 11
US-08-585-6848-130
Prd. No. 8-6e+03
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
ADDRESS: 15000 S. 1st Ave
CITY: Scottsdale, AZ
STATE: Arizona
COUNTRY: USA
ZIP: 85260
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM PC
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 08/08/97
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE: 08/08/97
FILING DATE: 08/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Saidwin, Geraldine G
REFERENCE/DOCKET NUMBER: 17,52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 868-9890
TELEFAX: (212) 868-9890
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDNESS: single
MOLUCULE TYPE: linear
FEATURE:
NAME/KEY: Modified Base
OTHER INFORMATION: Where N is any nucleotide
US-08-747-121-4

Query Match 100.0% Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Prd. No. 8-6e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGTATGA 7
DB 9 AGTATGA 3

```

1  NUMBER OF SEQUENCES: 2751
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Lyon & Lyon
4  STREET: 1450 14th Street
5  CITY: Suite 4700
6  STATE: Los Angeles
7  COUNTRY: U.S.A.
8  ZIP: 90071
9
10  COMPUTER READABLE FORM:
11  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
12  OPERATING SYSTEM: IBM PC DOS 5.0
13  CURRENT APPLICATION DATA:
14  ATTORNEY/AGENT INFORMATION:
15  NAME: Warburg, Richard
16  REGISTRATION NUMBER: 21327
17  TELEPHONE: (213) 489-1600
18  TELEFAX: (213) 955-0440
19  TELECOMMUNICATION INFORMATION:
20  REFERENCE/DOCKET NUMBER: 08/000.951
21  INFORMATION FOR SEQ ID NO: 1315:
22  SEQUENCE CHARACTERISTICS:
23  TYPE: nucleic acid
24  STRANDEDNESS: single
25  TOPOLOGY: linear
26  US-08-585-6848-1315
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28  Query Match 100.0%; Score 7; DB 2; Length 15;
29  Best Local Similarity 71.4%; Pred. No. 8.6e+03;
30  Matches 0; Mismatches 2; Indels 0; Gaps 0;
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32  Ov 1 AQUAVA 7
33  DB 5 AQUAVA 11
34
35  RESULT 13
36  US-08-485-113-28
37  Sequence 28; Application US/08485113
38  Patent No. 5976789
39  OPERATING SYSTEM:
40  APPLICANT: Allibert, Patrice A.
41  APPLICANT: Croes, Philippe
42  APPLICANT: Mach, Bernard F.
43  APPLICANT: Tiercy, Jean-Marie
44  TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING
45  TITLE OF INVENTION: METHOD AND REAGENT FOR THE
46  INDUCTION OF GRAFT TOLERANCE
47  NUMBER OF SEQUENCES: 61
48  CORRESPONDENCE ADDRESS:
49  ADDRESSEE: OLIFF & BERRIDGE
50  STREET: Old Dock 1928
51  CITY: Alexandria
52  STATE: Virginia
53  ZIP: 22320
54  COMPUTER READABLE FORM:
55  MEDIUM TYPE: Floppy disk
56  OPERATING SYSTEM: IBM PC compatible
57  CURRENT APPLICATION DATA:
58  ATTORNEY/AGENT INFORMATION:
59  NAME: Berridge, William P.
60  REGISTRATION NUMBER: 10140
61  REFERENCE/DOCKET NUMBER: WFB 28596A
62  TELECOMMUNICATION INFORMATION:
63  TELEPHONE: 703-936-6400
64  INFORMATION FOR SEQ ID NO: 28:
65  SEQUENCE CHARACTERISTICS:
66  TYPE: nucleic acid
67  LENGTH: 15 base pairs
68  TYPE: nucleic acid
69
70  Query Match 100.0%; Score 7; DB 2; Length 15;
71  Best Local Similarity 71.4%; Pred. No. 8.6e+03;
72  Matches 0; Mismatches 2; Indels 0; Gaps 0;
73
74  Ov 1 AQUAVA 7
75  DB 5 AQUAVA 11
76
77  RESULT 12
78  US-08-585-6848-1315
79  Sequence 1315; Application US/085856848
80  Patent No. 5976789
81  OPERATING SYSTEM:
82  APPLICANT: Stinchcomb, Daniel T.
83  APPLICANT: Mesiv, Thales
84  APPLICANT: Mesiv, Thales
85  TITLE OF INVENTION: METHOD AND REAGENT FOR THE
86  INDUCTION OF GRAFT TOLERANCE
87  TITLE OF INVENTION: METHOD AND REAGENT FOR THE
88  INDUCTION OF GRAFT TOLERANCE
89  NUMBER OF SEQUENCES: 2751
90  CORRESPONDENCE ADDRESS:
91  ADDRESSEE: Lyon & Lyon
92  STREET: 1450 14th Street
93  CITY: Suite 4700
94  STATE: Los Angeles
95  COUNTRY: U.S.A.
96  ZIP: 90071
97
98  COMPUTER READABLE FORM:
99  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
100  OPERATING SYSTEM: IBM PC DOS 5.0
101  CURRENT APPLICATION DATA:
102  ATTORNEY/AGENT INFORMATION:
103  NAME: Warburg, Richard
104  REGISTRATION NUMBER: 21327
105  TELEPHONE: (213) 489-1600
106  TELEFAX: (213) 955-0440
107  TELECOMMUNICATION INFORMATION:
108  REFERENCE/DOCKET NUMBER: 08/000.951
109  INFORMATION FOR SEQ ID NO: 130:
110  SEQUENCE CHARACTERISTICS:
111  TYPE: nucleic acid
112  STRANDEDNESS: single
113  TOPOLOGY: linear
114  US-08-585-6848-130
115
116  Query Match 100.0%; Score 7; DB 2; Length 15;
117  Best Local Similarity 71.4%; Pred. No. 8.6e+03;
118  Matches 0; Mismatches 2; Indels 0; Gaps 0;
119
120  Ov 1 AQUAVA 7
121  DB 5 AQUAVA 11
122
123  RESULT 12
124  US-08-585-6848-1315
125  Sequence 1315; Application US/085856848
126  Patent No. 5976789
127  OPERATING SYSTEM:
128  APPLICANT: Stinchcomb, Daniel T.
129  APPLICANT: Mesiv, Thales
130  APPLICANT: Mesiv, Thales
131  TITLE OF INVENTION: METHOD AND REAGENT FOR THE
132  INDUCTION OF GRAFT TOLERANCE
133  TITLE OF INVENTION: METHOD AND REAGENT FOR THE
134  INDUCTION OF GRAFT TOLERANCE
135  NUMBER OF SEQUENCES: 2751
136  CORRESPONDENCE ADDRESS:
137  ADDRESSEE: Lyon & Lyon
138  STREET: 1450 14th Street
139  CITY: Suite 4700
140  STATE: Los Angeles
141  COUNTRY: U.S.A.
142  ZIP: 90071
143
144  COMPUTER READABLE FORM:
145  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
146  OPERATING SYSTEM: IBM PC DOS 5.0
147  CURRENT APPLICATION DATA:
148  ATTORNEY/AGENT INFORMATION:
149  NAME: Warburg, Richard
150  REGISTRATION NUMBER: 21327
151  TELEPHONE: (213) 489-1600
152  TELEFAX: (213) 955-0440
153  TELECOMMUNICATION INFORMATION:
154  REFERENCE/DOCKET NUMBER: 08/000.951
155  INFORMATION FOR SEQ ID NO: 130:
156  SEQUENCE CHARACTERISTICS:
157  TYPE: nucleic acid
158  LENGTH: 15 base pairs
159  TYPE: nucleic acid

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STANDARDS: single
TOPOLGY: linear

Query Match 100.0%; Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Prod. No. 8.6e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGTATGA 7
Db 9 AGTATGA 15

RESULT 14
US-09-034-714A-33/c
Sequence 33; Application US/09094714A
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett, Nicholas M. Dean

TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
NAMES: POLYMERIZATION OF PROTEIN KINASE C EXPRESSION

NUMBER OF SEQUENCES: 69
CURRENT APPLICATION DATA: 08/08/094, 714A
FILING DATE: June 15, 1998

CLASSIFICATION: 435
PRIORITY APPLICATION DATA: 08/601,269

PRIOR APPLICATION DATA: 08/478,178
PRIORITY APPLICATION DATA: 07/JUN-1995

APPLICANT NUMBER: 08/089,996
APPLICATION NUMBER: 08/089,996

REGISTRATION NUMBER: 38,534
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33;
SEQUENCE CHARACTERISTICS:

LENGTH: 15
TYPE: nucleic acid
SYNTHESIS: single

TOPOLGY: linear

US-09-034-714A-33

Query Match 100.0%; Score 7; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 8.6e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGTATGA 7
Db 12 AGTATGA 6

RESULT 15
US-09-034-714A-34/c
Sequence 34; Application US/09094714A
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett, Nicholas M. Dean

TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
NAMES: POLYMERIZATION OF PROTEIN KINASE C EXPRESSION

NUMBER OF SEQUENCES: 69
CURRENT APPLICATION DATA: 08/08/094, 714A
FILING DATE: June 15, 1998

CLASSIFICATION: 435
PRIORITY APPLICATION DATA: 08/601,269

PRIOR APPLICATION DATA: 08/478,178
PRIORITY APPLICATION DATA: 07/JUN-1995

APPLICANT NUMBER: 08/089,996
APPLICATION NUMBER: 08/089,996

REGISTRATION NUMBER: 38,534
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 34;
SEQUENCE CHARACTERISTICS:

LENGTH: 15
TYPE: nucleic acid
SYNTHESIS: single

TOPOLGY: linear

US-09-034-714A-34

Query Match 100.0%; Score 7; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 8.6e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGTATGA 7
Db 14 AGTATGA 8

Search completed: January 1, 2004, 00:32:18
Job time : 27.3136 secs

GenCore version 5.1.6

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ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 839.57 Seconds
444,364 Million cell updates/sec

Title: US-09-540-843-1

Sequence: 1 gactgtagg g

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 288871 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 10 summaries

Database :

1: gb-hg-hum*

2: gb-hg-hum*

3: gb-hg-hum*

4: gb-hg-hum*

5: gb-hg-hum*

6: gb-hg-hum*

7: gb-hg-hum*

8: gb-hg-hum*

9: gb-hg-hum*

10: gb-hg-hum*

11: gb-hg-hum*

12: gb-hg-hum*

13: gb-hg-hum*

14: gb-hg-hum*

15: gb-hg-hum*

16: gb-hg-hum*

17: gb-hg-hum*

18: gb-hg-hum*

19: gb-hg-hum*

20: gb-hg-hum*

21: gb-hg-hum*

22: gb-hg-hum*

23: gb-hg-hum*

24: gb-hg-hum*

25: gb-hg-hum*

26: gb-hg-hum*

27: gb-hg-hum*

28: gb-hg-hum*

29: gb-hg-hum*

30: gb-hg-hum*

31: gb-hg-hum*

32: gb-hg-hum*

33: gb-hg-hum*

34: gb-hg-hum*

35: gb-hg-hum*

36: gb-hg-hum*

37: gb-hg-hum*

38: gb-hg-hum*

39: gb-hg-hum*

40: gb-hg-hum*

41: gb-hg-hum*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	6	AX268753 Sequence
2	9	100.0	10	6	AX571597 Sequence
3	9	100.0	10	6	AX571610 Sequence
4	9	100.0	10	6	AX571610 Sequence
5	9	100.0	15	6	AX110719 Sequence
6	9	100.0	15	6	AX110720 Sequence
7	9	100.0	17	6	AX039517 Sequence
8	9	100.0	17	6	AX039517 Sequence
9	9	100.0	17	6	AX039521 Sequence
10	9	100.0	17	6	AX039523 Sequence
11	9	100.0	17	6	AX651124 Sequence
12	9	100.0	17	6	AX651125 Sequence
13	9	100.0	17	6	AX651126 Sequence
14	9	100.0	17	6	AX651126 Sequence
15	9	100.0	17	6	AX651126 Sequence
16	9	100.0	17	6	AX651126 Sequence
17	9	100.0	17	6	AX651129 Sequence
18	9	100.0	17	6	AX651130 Sequence
19	9	100.0	17	6	AX651130 Sequence
20	9	100.0	17	6	AX651130 Sequence
21	9	100.0	19	6	AX709273 Sequence
22	9	100.0	20	6	AX116520 Sequence
23	9	100.0	20	6	AX116520 Sequence
24	9	100.0	20	6	AX116520 Sequence
25	9	100.0	20	6	AX229019 Sequence
26	9	100.0	20	6	AX229019 Sequence
27	9	100.0	20	6	AX229019 Sequence
28	9	100.0	20	6	AX556397 Sequence
29	9	100.0	20	6	AX573612 Sequence
30	9	100.0	20	6	AX573612 Sequence
31	9	100.0	20	6	AX573612 Sequence
32	9	100.0	20	6	AX573612 Sequence
33	9	100.0	20	6	AX573612 Sequence
34	9	100.0	20	6	AX573612 Sequence
35	9	100.0	21	6	AX039521 Sequence
36	9	100.0	21	6	AX039523 Sequence
37	9	100.0	22	6	AX338664 Sequence
38	9	100.0	22	6	AX338664 Sequence
39	9	100.0	24	6	AX431318 Sequence
40	9	100.0	25	6	AX454970 Sequence
41	9	100.0	25	6	AX631696 Sequence
42	9	100.0	25	6	AX631696 Sequence
43	9	100.0	25	6	AX631696 Sequence
44	9	100.0	25	6	AX631696 Sequence
45	9	100.0	25	6	AX631696 Sequence

ALIGNMENTS

RESULT 1	AX268753	8 bp	DNA
IDENTIFICATION	AX268753	1	From Patent WO0174312.
VERSION	AX268753.1	GI:16541825	
SOURCE	synthetic construct		
ORGANISM	artificial sequence		
REFERENCE	Gilchrist, B.A., Yarr, M. and Eller, M.		
AUTHORS	Use of locally applied dia fragments		
TITLE	Patent WO 0174312-A1 11-OCT-2001		
JOURNAL	INSTRUMENTS OF BOSTON UNIVERSITY (US)		

Prod. No. is the number of results predicted by chance to have a

FEATURES source Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Antibiotic-free DNA fragment"

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 ORIGIN 0 c 4 g 2 t
 Query Match 100.0%; Score 9; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.5e+09;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
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 Db 1 GAGTATGAG 9

RESULT 4
 AX573600.1 GI:27551270
 LOCUS AX573600.1 12 bp DNA linear PAT 07-JAN-2003
 DEFINITION Sequence 10 from Patent WO20079467.
 ACCESSION AX573600.1
 VERSION AX573600.1
 KEYWORDS synthetic construct
 SOURCE artificial sequences.
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Nielsen, P.E. and Good, L.
 TITLE Antibiotic-free bacterial strain selection with antisense molecules
 JOURNAL Location/Qualifiers
 COUNTRY Denmark
 ADDRESS Copenhagen University (DK)
 FEATURES source
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Antibiotic-free antisense oligonucleotide"

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 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
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 Db 9 GAGTATGAG 1

RESULT 3
 AX573610.1 GI:27551280
 LOCUS AX573610.1 10 bp DNA linear PAT 07-JAN-2003
 DEFINITION Sequence 20 from Patent WO20079467.
 ACCESSION AX573610.1
 VERSION AX573610.1
 KEYWORDS synthetic construct
 SOURCE artificial sequences.
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Nielsen, P.E. and Good, L.
 TITLE Antibiotic-free bacterial strain selection with antisense molecules
 JOURNAL Location/Qualifiers
 COUNTRY Denmark
 ADDRESS Copenhagen University (DK)
 FEATURES source
 1..10
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Peptide nucleic acid SP4"

BASE COUNT 1 a 10 c 10 g 10 t
 ORIGIN 1 a 10 c 10 g 10 t
 Query Match 100.0%; Score 9; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
 |||||
 Db 1 GAGTATGAG 9

RESULT 5
 AX573610.1 GI:27551280
 LOCUS AX573610.1 15 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 6 from patent US 6190866.
 ACCESSION AX573610.1
 VERSION AX573610.1
 KEYWORDS synthetic construct
 SOURCE artificial sequences.
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Nielsen, P.E. and Good, L.
 TITLE Methods of bacterial gene function determination using peptide
 JOURNAL Location/Qualifiers
 COUNTRY US
 ADDRESS Patent: US 6190866-A 6 20-FEB-2001;
 FEATURES source
 1..15
 /organism="unknown"
 /mol_type="unknown"

BASE COUNT 3 a 6 c 0 g 6 t
 ORIGIN 3 a 6 c 0 g 6 t
 Query Match 100.0%; Score 9; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9
 |||||
 Db 11 GAGTATGAG 3

NOTE="The polypeptide KFFKFFKFFK (SEQ ID NO:1) is linked to the C-terminal RNA sequence via the epsilon glycol linker called 'epi'."


```

Oy 1 GAGTATGAG 3
Db 11 GAGTATGAG 3

RESULT 6
AL130720/c
DEFINITION Sequence 7 from patent US 610886.
ACCESSION AR130720
VERSION AR130720.1 GI:14119045
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Nielsen, P.E. and Good, L.
TITLE Methods of bacterial gene function determination using peptide
JOURNAL Microb. Drug Resist. 7:20-FEB-2001.
FEATURES
    source 1..15
    location Location/Qualifiers
BASE COUNT 5 a 4 c 1 g 5 t
Query Match 100.0%; Score 9; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
Db 14 GAGTATGAG 6

RESULT 7
AR039517/c
DEFINITION Sequence 365 from patent US 5807743.
ACCESSION AR039517
VERSION AR039517.1 GI:5958880
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL JOURNAL OF CLINICAL INVESTIGATION
PATENT: US 5807743-A 365 15-SEP-1998;
FEATURES
    source 1..17
    location Location/Qualifiers
BASE COUNT 3 a 7 c 2 g 5 t
Query Match 100.0%; Score 9; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
Db 17 GAGTATGAG 9

RESULT 8
AR039519/c
LOCUS Sequence 367 from patent US 5807743.
DEFINITION AR039519
ACCESSION AR039519.1 GI:5958882
VERSION AR039519.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL JOURNAL OF CLINICAL INVESTIGATION
PATENT: US 5807743-A 371 15-SEP-1998;
FEATURES
    source 1..17
    location Location/Qualifiers
BASE COUNT 4 a 9 c 0 g 4 t
Query Match 100.0%; Score 9; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
Db 12 GAGTATGAG 4

RESULT 9
AR039521/c
LOCUS Sequence 371 from patent US 5807743.
DEFINITION AR039521
ACCESSION AR039521.1 GI:5958886
VERSION AR039521.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL JOURNAL OF CLINICAL INVESTIGATION
PATENT: US 5807743-A 369 15-SEP-1998;
FEATURES
    source 1..17
    location Location/Qualifiers
BASE COUNT 3 a 8 c 1 g 5 t
Query Match 100.0%; Score 9; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
Db 15 GAGTATGAG 7

RESULT 9
AR039521/c
LOCUS Sequence 369 from patent US 5807743.
DEFINITION AR039521
ACCESSION AR039521.1 GI:5958884
VERSION AR039521.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL JOURNAL OF CLINICAL INVESTIGATION
PATENT: US 5807743-A 369 15-SEP-1998;
FEATURES
    source 1..17
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BASE COUNT 3 a 8 c 1 g 5 t
Query Match 100.0%; Score 9; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
Db 15 GAGTATGAG 7

RESULT 9
AR039521/c
LOCUS Sequence 371 from patent US 5807743.
DEFINITION AR039521
ACCESSION AR039521.1 GI:5958886
VERSION AR039521.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL JOURNAL OF CLINICAL INVESTIGATION
PATENT: US 5807743-A 371 15-SEP-1998;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAGTATGAG 9
Db 9 GAGTATGAG 1

RESULT 11
LOCUS AX693123/c
DEFINITION AX693123: Homo sapiens
ACCESSION AX693123.1 GI:29416087
VERSION AX693123.1 GI:29416087
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Shannon M., Gu Y., and Nguyen C.T.
TITLE Four human zinc-finger-containing proteins : md23, md14, md17 and md12
JOURNAL Patent: EP 1281758-A 5856 05-FEB-2003;
Neomica, Inc. (US)
FEATURES
source Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 5 c 1 g 7 t

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Best Local Similarity 100.0%; Pred. No. 87e+04; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9
Db 17 GAGTATGAG 9

RESULT 12
LOCUS AX693124/c
DEFINITION AX693124: Homo sapiens
ACCESSION AX693124.1 GI:29416088
VERSION AX693124.1 GI:29416088
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Shannon M., Gu Y., and Nguyen C.T.
TITLE Four human zinc-finger-containing proteins : md23, md14, md17 and md12
JOURNAL Patent: EP 1281758-A 5856 05-FEB-2003;
Neomica, Inc. (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 3 a 5 c 1 g 8 t

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Best Local Similarity 100.0%; Pred. No. 87e+04; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9
Db 16 GAGTATGAG 8

RESULT 13
LOCUS AX693125/c
DEFINITION AX693125: Homo sapiens
ACCESSION AX693125.1 GI:29416089
VERSION AX693125.1 GI:29416089
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Shannon M., Gu Y., and Nguyen C.T.
TITLE Four human zinc-finger-containing proteins : md23, md14, md17 and md12
JOURNAL Patent: EP 1281758-A 5857 05-FEB-2003;
Neomica, Inc. (US)
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source Location/Qualifiers
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BASE COUNT 3 a 5 c 0 g 9 t

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 GAGTATGAG 7

RESULT 14
LOCUS AX693126/c
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ACCESSION AX693126.1 GI:29416090
VERSION AX693126.1 GI:29416090
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Shannon M., Gu Y., and Nguyen C.T.
TITLE Four human zinc-finger-containing proteins : md23, md14, md17 and md12
JOURNAL Patent: EP 1281758-A 5856 05-FEB-2003;
Neomica, Inc. (US)
FEATURES
source Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 3 a 5 c 0 g 9 t

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 GAGTATGAG 6

RESULT 15
LOCUS AX693127/c
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ACCESSION AX693127.1 GI:29416091
VERSION AX693127.1 GI:29416091
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Shannon M., Gu Y., and Nguyen C.T.
TITLE Four human zinc-finger-containing proteins : md23, md14, md17 and md12
JOURNAL Patent: EP 1281758-A 5857 05-FEB-2003;
Neomica, Inc. (US)
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9
Db 14 GAGTATGAG 6

RESULT 16
LOCUS AX693128/c
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ACCESSION AX693128.1 GI:29416092
VERSION AX693128.1 GI:29416092
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Shannon M., Gu Y., and Nguyen C.T.
TITLE Four human zinc-finger-containing proteins : md23, md14, md17 and md12
JOURNAL Patent: EP 1281758-A 5857 05-FEB-2003;
Neomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 5 c 0 g 9 t

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Db 14 GAGTATGAG 6

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VERSION      AX653127.1  GI:29416091
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SOURCE       UNOANISM
ORGANISM     Bacteria; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Shannon M., Gu Y. and Nguyen C.T.
AUTHORS      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE        mdz12
JOURNAL      Patent: EP 1281056-A 5859 05-FEB-2003;
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             3 a 5 c 1 g 8 t
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             Best Local Similarity 100.0%; Pred. No. 8.7e+04;
             Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
             1 GAGTATGAG 9
             |||||
             13 GAGTATGAG 5
             Search completed: December 31, 2003, 17:09:38
             CPU time : 030.57 secs

```


The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic,

XX

Copied from 09980559 on 05/19/200

PA (UYKO-) UNIV DORTMUND.

PI Nielsen PE, Good L;

XX WPI, 2003-103773/09.

XX Selecting genetically modified cells useful for isolation and

XX industrial growth of transformed organisms comprises treating the

XX industrial cell culture medium or antigen construct designed against

XX the essential gene X of the cells.

XX

XX Claim 29; Fig 1; 9pp; English.

XX The invention relates to selecting genetically modified cells comprising:

XX (a) modifying cells selecting a growth essential gene X, with a vector

XX containing gene Y; and (b) treating the modified cells with an antisense

XX compound to inhibit the growth of the modified cells over other non-

XX modified cells. Also included is a product manufactured fully or

XX partially by modified cells and methods for using the product for

XX research the isolation and industrial growth maintenance of transformed

XX organisms. The new method has the advantage of selecting and maintaining

XX genetically modified cells and manufacturing products. It is useful for

XX industrial production involving genetically modified micro-organisms. The

XX method inhibits bacterial infections in eukaryotic cell cultures used to

XX produce peptide nucleic acid (PNA) molecules that are converted into a

XX gene (gene X in this example).

XX

XX Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;

XX

XX Query Match 100.0%; Score 9; DB 25; Length 10;

XX Best Local Similarity 100.0%; Pred. No. 1,1e+04;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX 1 GAGTATGAG 9

XX 9 GAGTATGAG 1

XX

XX RESULT 5

XX ABI05192

XX ABI05192 standard; DNA, 12 BP.

XX

XX AB05192;

XX

XX 22-FEB-2002 (first entry)

XX

XX Oligonucleotide primer SEQ ID NO 305165 for detecting SNP TSC0021329.

XX

XX SNP; single nucleotide polymorphisms; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

XX Homo sapiens.

XX

XX WO20017384-A2.

XX

XX 18-OCT-2001.

XX

XX 06-APR-2001; 2001WO-1800713.

XX

XX 07-APR-2000; 2000DE-1019173.

XX

XX (EP10-) EPICENOMICS AG.

XX

XX Olek A, Piepenbrock C, Berlin K;

XX

XX WPI, 2001-657177/75.

XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single nucleotide polymorphisms and cytosine

XX methylation status

XX

XX Claim 1; SEQ ID 306811; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligomers are used in a range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation.

XX

XX AB00010-AB02073 represent the oligomers described in the invention.

XX

XX NOTE: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format from WFO at

XX ftp.wipo.int/pub/published_pat_sequences.

XX

XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 other;

XX

XX Query Match 100.0%; Score 9; DB 23; Length 12;

XX Best Local Similarity 100.0%; Pred. No. 1,1e+04;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX 1 GAGTATGAG 9

XX 1 GAGTATGAG 9

XX

XX RESULT 7

XX ABI06838

XX ABI06838 standard; DNA, 12 BP.

XX

XX AB06838;

XX

XX 22-FEB-2002 (first entry)

XX

XX Oligonucleotide primer SEQ ID NO 306811 for detecting SNP TSC0022179.

XX

XX SNP; single nucleotide polymorphisms; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

XX Homo sapiens.

XX

XX WO20017384-A2.

XX

XX 18-OCT-2001.

XX

XX 06-APR-2001; 2001WO-1800713.

XX

XX 07-APR-2000; 2000DE-1019173.

XX

XX (EP10-) EPICENOMICS AG.

XX

XX Olek A, Piepenbrock C, Berlin K;

XX

XX WPI, 2001-657177/75.

XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single nucleotide polymorphisms and cytosine

XX methylation status

XX

XX Claim 1; SEQ ID 306811; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligomers are used in a range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation.

XX

XX AB00010-AB039999, AB03010-AB039999, AB00010-AB039999 and

CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 other;
 CC Query Match 100.0%; Score 9; DB 23; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 1.1e-04;
 CC Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
 3 GAGTATGAG 11

CC RESULT 8
 CC AB106839
 CC AB106839 standard; DNA; 12 BP.
 CC AB106839;
 CC AB106839;

CC 22-FEB-2002 (first entry)
 CC Oligonucleotide primer SEQ ID NO 306812 for detecting SNP TSC022179.
 CC SNP; single nucleotide polymorphism; human; diagnosis; RNA; cancer; CNS;
 CC peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
 CC central nervous system; gastrointestinal; respiratory; immune; metabolic.
 CC Homo sapiens.

CC MO200177384-A2.
 CC 18-OCT-2001.
 CC 06-APR-2001; 2001WO-1800713.
 CC 07-APR-2000; 2000DE-1019173.
 CC (EPIG-) EPIGENOMICS AG.

CC Olek A, Plegenbrock C, Berlin K;
 CC WPI; 2001-657177/5.
 CC Set of oligonucleotides, useful for diagnosis and cell typing, is
 CC designed to detect single nucleotide polymorphisms and cytosine
 CC methylation status

CC Claim 1; SEQ ID 306812; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomer are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABP00010-ABP99989, AHH00010-AHH99989 and
 CC ABC00010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 other;
 CC Query Match 100.0%; Score 9; DB 23; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 1.1e-04;
 CC Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
 1111111111

Db 3 GAGTATGAG 11
 CC RESULT 9
 CC AB121133
 CC AB121133 standard; DNA; 12 BP.
 CC AB121133;
 CC AB121133;
 CC 22-FEB-2002 (first entry)

CC Oligonucleotide primer SEQ ID NO 321106 for detecting SNP TSC030074.
 CC SNP; single nucleotide polymorphism; human; diagnosis; RNA; cancer; CNS;
 CC peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
 CC central nervous system; gastrointestinal; respiratory; immune; metabolic.

CC Homo sapiens.
 CC WQ3000177384-A2.
 CC 18-OCT-2001.
 CC 06-APR-2001; 2001WO-1800713.
 CC 07-APR-2000; 2000DE-1019173.
 CC (EPIG-) EPIGENOMICS AG.

CC Olek A, Plegenbrock C, Berlin K;
 CC WPI; 2001-657177/5.
 CC Set of oligonucleotides, useful for diagnosis and cell typing, is
 CC designed to detect single nucleotide polymorphisms and cytosine
 CC methylation status

CC Claim 1; SEQ ID 321106; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABP00010-ABP99989, AHH00010-AHH99989 and
 CC ABC00010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 other;
 CC Query Match 100.0%; Score 9; DB 23; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 1.1e-04;
 CC Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGTATGAG 9
 2 GAGTATGAG 10

CC RESULT 10
 CC AB126099
 CC AB126099 standard; DNA; 12 BP.
 CC AB126099;
 CC AB126099;

CC 22-FEB-2002 (first entry)
 CC Oligonucleotide primer SEQ ID NO 326072 for detecting SNP TSC032886.

CC

modified_base 12 derived from an unknown amino acid"
 FT FT /tag= e OTHER
 FT FT /mod=OTHER
 FT FT /note=OTHER
 FT FT N-(2-Boc-aminoethyl)-N-(chymine-1-yl-acetyl)lysine
 FT FT and is a C-terminal aside"
 PK XX HQ020253574-A2.
 11-JUL-2002.
 PP PD 03-JAN-2002; 2002MO-DKG00005.
 XX XX 05-JAN-2001; 2001DK-0000021.
 PK XX (PANT-) PANTHECO AS.
 XX XX Nielsen PE, Manoharan M, Puschl A;
 XX MF1; 2002-575409/61.
 XX XX New peptide nucleic acid monomer useful e.g. in the treatment of
 XX immunological disorders
 XX Example 1; Page 23; 9pp; English.
 CC The invention discloses peptide nucleic acid (PNA) monomers which can be
 CC used to combat diseases, especially bacterial infections, by targeting
 CC molecules such as 23S ribosomal RNA and inhibiting translation. They are
 CC e.g. bacterial and viral infections, cardiac or vascular diseases,
 CC metabolic diseases (e.g. diabetes or inborn errors of metabolism) and
 CC immunological disorders. (e.g. microorganisms that can be inhibited include
 CC Bacillus, Listeria, Clostridium, Propionibacterium), Gram-negative
 CC bacteria (e.g. Bacteroides, Fusobacterium, Escherichia, Klebsiella,
 CC Hemophilus, Bordetella, Brucella, Campylobacter, Neisseria, Brucella),
 CC and organisms which stain poorly with Gram's stain (e.g. Mycobacterium,
 CC Treponema, Leptospira, Borrelia, Mycoplasma, Chlamydia, Rickettsia,
 CC and other microorganisms). The sequence presented in the modified PNA molecule, #8
 CC effect with different orientation of the peptide in relation to the
 CC PNA-sequence. The sequence presented in the modified PNA molecule, #8
 CC (AM91039) complementary DNA sequence.
 XX Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 other;
 Query Match 100.0%; Score 9; DB 24; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e-04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGTATGAG 9
 DB 11 GAGTATGAG 9
 RESULT 13
 ID ASK51039 standard; DNA; 12 BP.
 AC ASK51039;
 XX 15-NOV-2002 (first entry)
 DE Modified peptide nucleic acid (PNA) molecule #8 complementary DNA.
 XX Peptide nucleic acid; PNA; bacterial infection; 23S ribosomal RNA; rRNA;
 XX translation; viral infection; cardiac disease; vascular disease;
 XX metabolic disease; diabetes; metabolism; immunological disorder;
 XX Gram-positive; Gram-negative; antineoplastic; as.
 XX Unidentified.

PK HQ020253574-A2.
 XX 11-JUL-2002.
 PP PD 03-JAN-2002; 2002MO-DKG00005.
 XX XX 05-JAN-2001; 2001DK-0000021.
 PK XX (PANT-) PANTHECO AS.
 XX XX Nielsen PE, Manoharan M, Puschl A;
 XX MF1; 2002-575409/61.
 XX XX New peptide nucleic acid monomer useful e.g. in the treatment of
 XX immunological disorders
 XX Example 1; Page 23; 9pp; English.
 CC The invention discloses peptide nucleic acid (PNA) monomers which can be
 CC used to combat diseases, especially bacterial infections, by targeting
 CC molecules such as 23S ribosomal RNA and inhibiting translation. They are
 CC e.g. bacterial and viral infections, cardiac or vascular diseases,
 CC metabolic diseases (e.g. diabetes or inborn errors of metabolism) and
 CC immunological disorders. (e.g. microorganisms that can be inhibited include
 CC Bacillus, Listeria, Clostridium, Propionibacterium), Gram-negative
 CC bacteria (e.g. Bacteroides, Fusobacterium, Escherichia, Klebsiella,
 CC Hemophilus, Bordetella, Brucella, Campylobacter, Neisseria, Brucella),
 CC and organisms which stain poorly with Gram's stain (e.g. Mycobacterium,
 CC Treponema, Leptospira, Borrelia, Mycoplasma, Chlamydia, Rickettsia,
 CC and other microorganisms). The sequence presented in the modified PNA molecule, #8
 CC effect with different orientation of the peptide in relation to the
 CC PNA-sequence. The sequence presented in the modified PNA molecule, #8
 CC (AM91039) complementary DNA sequence.
 XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 other;
 Query Match 100.0%; Score 9; DB 24; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e-04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGTATGAG 9
 DB 2 GAGTATGAG 10
 RESULT 14
 ID ASK51040 standard; RNA; 12 BP.
 AC ASK51040;
 XX 15-NOV-2002 (first entry)
 DE Modified peptide nucleic acid (PNA) molecule #8 complementary RNA.
 XX Peptide nucleic acid; PNA; bacterial infection; 23S ribosomal RNA; rRNA;
 XX translation; viral infection; cardiac disease; vascular disease;
 XX metabolic disease; diabetes; metabolism; immunological disorder;
 XX Gram-positive; Gram-negative; antineoplastic; as.
 XX Unidentified.
 XX HQ020253574-A2.
 XX 11-JUL-2002.
 PP PD 03-JAN-2002; 2002MO-DKG00005.

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tcna_protocol.html

BASE COUNT 6 a 10 c 4 g
Query Match 100.0%; Score 9; DB 28; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATG 9
22 GAGTATG 14

RESULT 4
LOCUS AM059679/c 24 bp mRNA linear EST 23-ADG-2000
DEFINITION AM059679.1 Homo sapiens CDNA, mRNA sequence.
VERSION AM059679.1 GI:6652001

KEYWORDS EST, sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Brenner, S., Williams, S.R., Verma, P.H., Storek, T., Moon, K., McCollum, C., Mao, J.T., Kirchner, J.J., Elet, S., DuRoi, R.B., Burman, T., and Albrecht, G.
A mixture of differentially expressed cDNAs separation of differentially expressed cDNAs on microbeads: Physical

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
PUBMED 2014498

COMMENT Contact: Burcham TS
LNK Therapeutics, Inc.
7861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 5300
Fax: 510 670 5302

EMAIL: tbls@lynken.com
Collected from LNK Therapeutics Megasort technology.
Collected from unamplified gate.

High quality sequence stop: 24.
Location/Qualifiers

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="THP-1 (T19-202)"
/clone_lib="DNC15"
/note="vector: pcR2.1; Cloning of PCR products from cells non-induced (treated with DMSO only)."

BASE COUNT 9 a 6 c 1 g 8 t
Query Match 88.9%; Score 8; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATG 8
24 GAGTATG 17

RESULT 5
LOCUS A2478673 24 bp DNA linear GSS 04-OCT-2000
DEFINITION 190298J20R Mouse 10kb plasmid UGCLM library Mus musculus genomic
Clone UGCLM190298J20 R, genomic survey sequence.
ACCESSION A2478673

VERSION M219673.1 GI:10637794
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Ayagi, A., Barber, M., Duval, B., Hamil, C., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A., and Wright, D., Weis, R.
Mouse 10kb genome scaffolding with paired end reads from 10kb plasmid UGCLM190298J20 R, genomic survey sequence.

JOURNAL Unpublished
COMMENT Contact: Robert B. Weis
University of Utah
Genome Center
Rm. 300, Biomedical Polymers Research Bldg., 20 S. 2010 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: dunn@genetics.utah.edu
Insert length: 10000
Seq primer: CACAGCAAGACCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

Location/Qualifiers
source
/organism="Mus musculus"
/mol_type="plasmid DNA"
/db_xref="taxon:10090"
/clone_lib="UGCLM190298J20"

/lab_name="E. coli strain XL10-Gold, TI-resistant, P-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="vector: PM22mv, Purified genomic DNA from M. laboratory Mouse DNA Resources
(<http://www.jax.org/resources/documents/dares/>). The DNA was hydrodynamically sheared by repeated passage through a needle and ligated into the blunt-ended UGCLM library DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The library was then size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of the library by digestion with the appropriate restriction enzyme. The construct was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to the blunt ends of the library DNA. The library was then chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 3 g 7 t
Query Match 88.9%; Score 8; DB 28; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AGTATG 9
8 AGTATG 1

RESULT 6
LOCUS A2605844/c 25 bp DNA linear GSS 13-DEC-2000
DEFINITION 190427J22F Mouse 10kb plasmid UGCLM library Mus musculus genomic
Clone UGCLM190427J22 F, genomic survey sequence.

Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
 SOURCE

1 30
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-215C11-014144"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /vector="pAC161". The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 amplification of the T-DNA insertion site are flanked by
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequences were
 processed for submission. T-DNA derived sequences were
 screened.

BASE COUNT 11 a 5 c 4 g 10 t

ORIGIN

Query Match 88.9%, Score 8, DB 29, Length 30;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATCA 8
 |||||
 19 GAGTATCA 26

RESULT 9
 DEFINITION HNC23-1-ELU.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION B0924068
 VERSION B0924068.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 17), R. Dadds B.A. Halsey, K. Van Horn, M. Mao J.,
 Satch, G. M. P. Agarwal, P. Badger, A.M., Lee, J.C., Gowen, M. and
 Lark, M.W.
 Identification and initial characterization of 5000 expressed
 sequence tags (ESTs) from human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 11597137
 Contact: Sanjay Kumar
 UW2109
 709 Swedish Road, P.O. Box 1559, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: skumar@legh.com
 Seq primer: 77
 Location/Qualifiers
 1..17
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /issue_type="cartilage"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 Directional"

BASE COUNT 2 a 10 c 0 g 5 t

Query Match 88.9%, Score 8, DB 29, Length 30;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATCA 8
 |||||
 19 GAGTATCA 26

RESULT 9
 DEFINITION HNC23-1-ELU.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION B0924068
 VERSION B0924068.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 17), R. Dadds B.A. Halsey, K. Van Horn, M. Mao J.,
 Satch, G. M. P. Agarwal, P. Badger, A.M., Lee, J.C., Gowen, M. and
 Lark, M.W.
 Identification and initial characterization of 5000 expressed
 sequence tags (ESTs) from human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 11597137
 Contact: Sanjay Kumar
 UW2109
 709 Swedish Road, P.O. Box 1559, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: skumar@legh.com
 Seq primer: 77
 Location/Qualifiers
 1..17
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /issue_type="cartilage"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 Directional"

BASE COUNT 2 a 10 c 0 g 5 t

ORIGIN

Query Match 82.2%, Score 7.4, DB 12, Length 17;
 Best Local Similarity 88.9%; Pred. No. 3.8e-05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GAGTATCA 9
 |||||
 13 GAGTATCA 5

RESULT 10
 DEFINITION U21805.21 Sugano mouse embryo nus mus musculus cDNA clone
 A1747751
 POLYADENYLATION SPECIFICITY FACTOR PROTEIN 1, cDNA sequence.
 A1747751 1 GI:5126015
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sotrogomata; Muridae; Murinae; Mus.
 1 (bases 1 to 19),
 Marra, M., Hillier, L., Kubista, T., Martin, J., Beck, C., Wylie, T.,
 Boudreau, N., Stojanovic, M., Mesing, B., Allen, M., Sowers, E.,
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Hesterton, R. and Wilson, R.
 Metastasis
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Unpublished
 JOURNAL
 COMMENT Washington University School of Medicine
 660 South Euclid Avenue, Box 8301, St. Louis, MO 63109, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 This manuscript was submitted to the IMAGE Consortium (image.lln.gov) for further information.
 MD: 995933
 Considered overall poor quality
 Possibility of contamination on wrong strand
 Seq primer: custom primer used
 High quality sequence stop: 1.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE2088248"
 /dev_stage="embryo, 14 dpc"
 /clone_lib="Sugano mouse embryo sews"
 /note="Vector: pME18s-FL3; Site 1: DraIII (CACTGCTGTC);
 Site 2: DraIII (CACTGCTGTC);
 double-stranded cDNA was ligated to a DraIII adaptor
 (TTTGGCCACTGTC), digested and cloned into distinct DraIII
 CACTGCTGTC. XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Suslo Sugano
 and Dr. Suslo Sugano.
 Custom primers for sequencing 5' and primer
 CTTCTGCTTAAGACTGG and 3' end primer
 CACTGCTGCTGCACTGCA." 3 t
 6 a 2 c 8 g 3 t

BASE COUNT 8 a 2 c 8 g 3 t

Query Match 82.2%, Score 7.4, DB 9, Length 19;
 Best Local Similarity 88.9%; Pred. No. 4e-05;

```

Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;
QY      1  GAGTATGAG  9
      |||||
Db      11  GAGTATG  19

RESULT 11
LOCUS      AZ45799/c
DEFINITION  IN010142P Mouse 10kb plasmid UUCGM library Mus musculus genomic
Clone UUCGM10101K12 F, genomic survey sequence.
ACCESSION  AZ45799
VERSION    AZ45799.1 GI:10472356
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  Bukacynska, M.; Nakazawa, S.; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Mammals; Sci. 19.
AUTHORS    Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiser, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished
COMMENT    Contact: Robert B. Weiser
University of Utah
Department of Human Genetics
3000 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
E-mail: rweiser@genetics.utah.edu
Insert length: 10000 Std error: 0.00
Plate: 0101 Row: K Column: 12
Seq primer: CCGTTTAAAGACGCGACGAT
High quality sequence stop: 19.
Location/Qualifiers
1..19
+/-name="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD22 (G11473214) (pB1A212972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with the sheared complementary DNA and adaptors and
purified. The sheared complementary DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.
5 a 4 c 8 a 5 c 6 t
BASE COUNT
ORIGIN
Query Match 82.2%; Score 7.41; DB 28; Length 19;

```



```

ORIGIN
Query Match      82.24; Score 7.4; DB 28; Length 20;
Best Local Similarity 88.94; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGTATGAG 9
|||||
DB 9 GAGTATGAG 17
|||||

```

```

BASE COUNT      4 a      1 c      8 g      8 t
ORIGIN
Query Match      82.24; Score 7.4; DB 28; Length 21;
Best Local Similarity 88.94; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGTATGAG 9
|||||
DB 13 GAGTATGAG 21
|||||

```

Search completed, December 31, 2003, 19:41:09
Job time : 1039.09 secs

```

RESULT 15
LOCUS      21 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M064805R Mouse 10kb Plasmid U9C1M library Mus musculus genomic
clone U9C2M064805 R, genomic survey sequence.
VERSION    AZ806440.1 GI:12969789
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

Bukarycia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Accession: G011111.1, Barber M., Beacorn T., Duval B., Hamil C.,
Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T., Reilly
M., Rose M., Rose R., Stokes R., Tingey A., von Niederhausen A.,
Ward M., White R., White R., White R., White R., White R., White R.,
Mus whole genome scaffolding with paired and reads from 10kb
plasmid inserts

```

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Unpublished
Author(s)  Robert B. Weiss
Institution University of Utah
Address     3065 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
City       Salt Lake City, UT 84143
Country    US
Tel        801 585 5606
Fax        801 585 7177
E-mail     robert.weiss@utah.edu
Insert Length 10000
Seq primer: CAGCAGGAACGACTGACCC
Seq primer: CAGCAGGAACGACTGACCC
High quality sequence stop: 21.
Location/Qualifiers
1..21
1. "lab.host"="S. Coli strain XL10-Gold, Tl-resistant, F-
2. "clonetype"="plasmid"
3. "clonetype"="plasmid"
4. "clonetype"="plasmid"
5. "clonetype"="plasmid"
6. "clonetype"="plasmid"
7. "clonetype"="plasmid"
8. "clonetype"="plasmid"
9. "clonetype"="plasmid"
10. "clonetype"="plasmid"
11. "clonetype"="plasmid"
12. "clonetype"="plasmid"
13. "clonetype"="plasmid"
14. "clonetype"="plasmid"
15. "clonetype"="plasmid"
16. "clonetype"="plasmid"
17. "clonetype"="plasmid"
18. "clonetype"="plasmid"
19. "clonetype"="plasmid"
20. "clonetype"="plasmid"
21. "clonetype"="plasmid"

```

```

FEATURES
source
1..21
1. "lab.host"="S. Coli strain XL10-Gold, Tl-resistant, F-
2. "clonetype"="plasmid"
3. "clonetype"="plasmid"
4. "clonetype"="plasmid"
5. "clonetype"="plasmid"
6. "clonetype"="plasmid"
7. "clonetype"="plasmid"
8. "clonetype"="plasmid"
9. "clonetype"="plasmid"
10. "clonetype"="plasmid"
11. "clonetype"="plasmid"
12. "clonetype"="plasmid"
13. "clonetype"="plasmid"
14. "clonetype"="plasmid"
15. "clonetype"="plasmid"
16. "clonetype"="plasmid"
17. "clonetype"="plasmid"
18. "clonetype"="plasmid"
19. "clonetype"="plasmid"
20. "clonetype"="plasmid"
21. "clonetype"="plasmid"

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 Search time 34.9777 Seconds
(without alignment)
113,581 Million cell updates/sec

Title: US-09-540-843-1
Perfect score: 1 gactatag 9
Sequence: 1 gactatag 9
Scoring table: IDENTITY.NUC
Gapop 10.0, Gapext 1.0

Searched: 56978 seqs, 226691566 residues
Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 30
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 1 Issued Patents NA+
2: /csm2/6/products/1/naa/5b COMB seq+
3: /csm2/6/products/1/naa/6a COMB seq+
4: /csm2/6/products/1/naa/7a COMB seq+
5: /csm2/6/products/1/naa/8a COMB seq+
6: /csm2/6/products/1/naa/backfiles1.seq+

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the hit.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	9	100.0	3	US-09-048-927-1	Sequence 1, Appli
2	9	100.0	15	US-09-049-190-6	Sequence 6, Appli
3	9	100.0	15	US-09-049-190-7	Sequence 7, Appli
4	9	100.0	15	US-08-932-140C-7	Sequence 7, Appli
5	9	100.0	15	US-08-932-140C-7	Sequence 7, Appli
6	9	100.0	17	US-08-758-306-365	Sequence 365, App
7	9	100.0	17	US-08-758-306-365	Sequence 365, App
8	9	100.0	17	US-08-758-306-365	Sequence 365, App
9	9	100.0	17	US-08-758-306-371	Sequence 371, App
10	9	100.0	20	US-09-287-796-101	Sequence 101, App
11	9	100.0	20	US-09-130-616-101	Sequence 101, App
12	9	100.0	20	US-09-130-616-102	Sequence 102, App
13	9	100.0	20	US-09-130-616-102	Sequence 102, App
14	9	100.0	20	US-09-105-059C-15	Sequence 15, Appli
15	9	100.0	20	US-09-105-059C-15	Sequence 15, Appli
16	9	100.0	20	US-09-517-467B-84	Sequence 84, Appli
17	9	100.0	20	US-09-422-978-6551	Sequence 6551, Ap
18	9	100.0	21	US-09-422-978-6551	Sequence 6551, Ap
19	9	100.0	21	US-09-422-978-6551	Sequence 6551, Ap
20	9	100.0	23	US-09-088-274-8	Sequence 8, Appli
21	9	100.0	24	US-09-245-248B-23	Sequence 23, Appli
22	9	100.0	24	US-09-912-485D-32	Sequence 32, Appli
23	9	100.0	27	US-09-031-006-4	Sequence 4, Appli
24	9	100.0	28	US-08-744-905A-4	Sequence 4, Appli
25	8	88.9	14	US-08-334-867-24	Sequence 24, Appli
26	8	88.9	15	US-08-747-421-4	Sequence 4, Appli
27	8	88.9	15	US-08-747-421-4	Sequence 4, Appli

29 8 88.9 15 US-08-585-684B-1315
Sequence 1315, Ap
30 8 88.9 16 US-07-977-284A-59
Sequence 59, Appli
c 31 8 88.9 16 US-08-256-126B-59
Sequence 59, Appli
32 8 88.9 17 US-08-995-162-444
Sequence 444, App
33 8 88.9 17 US-08-995-162-444
Sequence 444, App
34 8 88.9 18 US-07-688-152C-8
Sequence 8, Appli
35 8 88.9 18 US-08-363-955-5
Sequence 5, Appli
36 8 88.9 18 US-08-363-955-5
Sequence 5, Appli
37 8 88.9 18 US-08-474-719C-8
Sequence 8, Appli
38 8 88.9 18 US-09-213-768-29
Sequence 29, Appli
39 8 88.9 18 US-09-213-768-29
Sequence 29, Appli
40 8 88.9 18 US-08-206-188B-8
Sequence 8, Appli
41 8 88.9 18 US-09-630-706-80
Sequence 80, Appli
c 42 8 88.9 18 US-09-167-109-21
Sequence 21, Appli
43 8 88.9 18 US-09-422-978-4729
Sequence 4729, Ap
c 44 8 88.9 18 US-09-422-978-4729
Sequence 4729, Ap
45 8 88.9 18 5 PCT-US81-02714-8
Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-048-927-1
Sequence 1, Application US/09048927
US-09-048-927-1
GENERAL INFORMATION:
APPLICANT: GlaxoSmithKline
APPLICANT: Vitar, Mita
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER PUBLICATION NUMBER: 08/467,012
EARLIER FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 9
SEQ ID NO: 9
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: DNA Fragment
US-09-048-927-1
Query Match
Ref. Local Similarity 100.0%; Score 9; DB 3; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGTATAG 9
db 1 GAGTATAG 9
RESULT 2
US-09-049-190-6/c
Sequence 6, Application US/09049190
US-09-049-190-6/c
Patent No. 6190866
GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Anticardiolipin Nucleic Acids Having
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.

ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/049.190
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: John N. Caldwell
 REGISTRATION NUMBER: 28,937
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION CHARACTERISTICS: 6:
 LENGTH: 15 bases
 STANDARDS: Genetic
 TOPOLOGY: linear
 FEATURE/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 2
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 3
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 7
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 8
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 9
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 12
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 13
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 14
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE/NAME/KEY: Modified-site
 LOCATION: 15
 OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-Lysine-glycine
 OTHER INFORMATION: backbone
 US-09-049-190-5

Query Match: 100.0% Score: 9; DE: 3; Length: 15;
 Matched: 15; Similarity: 100.0%; Mismatches: 0;
 Matched: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 Qy: 11 GAGTATG 9
 Db: 11 GAGTATG 3
 RESULT 3
 US-09-049-190-7/c
 Sequence 7: Application US/09049190
 PENDING INFORMATION:
 GENERAL INFORMATION:
 APPLICANT: Nielsen et al.
 TITLE OF INVENTION: Peptide Nucleic Acids Having
 Nucleic Acid Mimetic Activity
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESS: Woodcock Winburn Nuts Mackiewicz
 CITY: Philadelphia
 STATE: PA 19103
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/049.190
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: John N. Caldwell
 REGISTRATION NUMBER: 28,937
 REFERENCE/DOCKET NUMBER: ISIS-2560
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100

& No. 6190866srls LLP

TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 2
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 7
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 8
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 9
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 12
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 13
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:

NAME/KEY: Modified-site
 LOCATION: 14
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 15
 OTHER INFORMATION: N-acetyl(2-aminoethyl)-C-lysine-glycine
 OTHER INFORMATION: backbone
 Query Match 100.0%; Score 0; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGTATGAG 9
 DB 14 GAGTATGAG 6
 RESULT 4
 US-08-932-140C-6/c
 Sequence 6; Application US/08932140C
 GENERAL INFORMATION:
 APPLICANT: Nielsen et al.
 TITLE OF INVENTION: Nucleic Acids Having
 Nucleic Acid Backbone Activity
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS: Hahnemann Kurtz Mackiewicz &
 Associates, P.C.
 ADDRESS: No. 6100181818 LRP
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER FILEABLE FORM
 MEDIUM TYPE: 3.5 inch disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/932,140C
 FILING DATE: September 16, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 AT NAME: John W. Caldwell
 REGISTRATION NUMBER: 28,937
 REFERENCE/LOCUT NUMBER: 1515-2560
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 LENGTH: 15 bases
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 2
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 7
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 8
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 9
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 12
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 13
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 14
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 15

1 LOCATION: 9
 2 OTHER INFORMATION: N-acetyl(2-aminoethy)glycine
 3 OTHER INFORMATION: backbone
 4 NAME/KEY: Modified-site
 5 LOCATION: 10
 6 OTHER INFORMATION: N-acetyl(2-aminoethy)glycine
 7 OTHER INFORMATION: backbone
 8 FEATURE:
 9 NAME/KEY: Modified-site
 10 LOCATION: 11
 11 OTHER INFORMATION: N-acetyl(2-aminoethy)glycine
 12 OTHER INFORMATION: backbone
 13 FEATURE:
 14 NAME/KEY: Modified-site
 15 LOCATION: 12
 16 OTHER INFORMATION: N-acetyl(2-aminoethy)glycine
 17 OTHER INFORMATION: backbone
 18 NAME/KEY: Modified-site
 19 LOCATION: 13
 20 OTHER INFORMATION: N-acetyl(2-aminoethy)glycine
 21 OTHER INFORMATION: backbone
 22 FEATURE:
 23 NAME/KEY: Modified-site
 24 LOCATION: 14
 25 OTHER INFORMATION: N-acetyl(2-aminoethy)glycine
 26 OTHER INFORMATION: backbone
 27 FEATURE:
 28 NAME/KEY: Modified-site
 29 LOCATION: 15
 30 OTHER INFORMATION: N-acetyl(2-aminoethy)glycine
 31 OTHER INFORMATION: backbone
 32 OTHER INFORMATION: lysine-glycine backbone
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 34 Query Match 100.0%; Score 9; DB 4; Length 15;
 35 Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
 36 Matches 9; Conservative 0; Mismatches 0;
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 38 1 GAGTATGAG 9
 39 14 GAGTATGAG 6
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SEQUENCE CHARACTERISTICS:

LENGTH 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: linear
 US-08-758-306-367

Query Match 100.0% Score 9; DB 1; Length 17;
 Best Local Similarity 100.0%; Prd. No. 1.5e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GAGTATGAG 9
 Db 15 GAGTATGAG 7

US-08-758-306-369/C
 Sequence 369, Application US/08759306
 Patent No. 5807743
 GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.
 TITLE OF INVENTION: REAGENT FOR THE
 TITLES OF INVENTION: TREATMENT OF DISEASES
 TITLE OF INVENTION: ASSOCIATED WITH
 INTERLEUKIN-2 RECEPTOR
 TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
 NUMBER OF SEQUENCES: 1379
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM: sheets, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: PASCAL Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,306
 FILING DATE: December 3, 1996
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 369:

SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-758-306-369

Query Match 100.0% Score 9; DB 1; Length 17;
 Best Local Similarity 100.0%; Prd. No. 1.5e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Qy 1 GAGTATGAG 9
 Db 12 GAGTATGAG 4

RESULT 9

US-08-758-306-371/C
 Sequence 371, Application US/08759306
 Patent No. 5807743
 GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.
 TITLE OF INVENTION: REAGENT FOR THE
 TITLES OF INVENTION: TREATMENT OF DISEASES
 TITLE OF INVENTION: ASSOCIATED WITH
 INTERLEUKIN-2 RECEPTOR
 TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
 NUMBER OF SEQUENCES: 1379
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.1" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: PASCAL Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,306
 FILING DATE: December 3, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 371:

SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-758-306-371

Query Match 100.0% Score 9; DB 1; Length 17;
 Best Local Similarity 100.0%; Prd. No. 1.5e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GAGTATGAG 9
 Db 9 GAGTATGAG 1

RESULT 10

US-09-287-796-101
 Sequence 101, Application US/09287796A
 Patent No. 5807743
 GENERAL INFORMATION:

APPLICANT: McKay, Robert A.
 TITLE OF INVENTION: TREATMENT OF DISEASES
 TITLE OF INVENTION: ASSOCIATED WITH
 INTERLEUKIN-2 RECEPTOR
 TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
 NUMBER OF SEQUENCES: 1379
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.1" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: PASCAL Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,306
 FILING DATE: December 3, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 371:

SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-758-306-371

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1 FILE REFERENCE: ISPH-0150
2 CURRENT APPLICATION NUMBER: US/09/287,796A
3 EARLIER FILING DATE: 1993-04-07
4 EARLIER APPLICATION NUMBER: 09/130,616
5 EARLIER FILING DATE: 1998-08-07
6 EARLIER APPLICATION NUMBER: 08/910,629
7 EARLIER FILING DATE: 1998-08-03
8 EARLIER APPLICATION NUMBER: 08/910,629
9 EARLIER FILING DATE: 1998-08-03
10 NUMBER OF SEQ ID NOS: 165
11 SEQ ID NO 101
12 LENGTH: 20
13 TYPE: DNA
14 ORGANISM: Artificial Sequence
15 FEATURES:
16 OTHER INFORMATION: Synthetic Sequence
17 US-09-287-796-101
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19 Query Match 100.0%; Score 9; DB 3; Length 20;
20 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
21 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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25 9 GAGTATGAG 17
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CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
CURRENT SEQ ID NOS: 28
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 15
LENGTH: 20
SEQUENCE:
GGATTCAG
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Forward primer
of Interleukin 12 p40 gene. From EST sequence similar to the X1421 gene
US-09-105-058C-15

Query Match
Accession No. US09105058C.1 100.0%; Score 9; DB 4; Length 20;
Matched Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGATTCAG 9
1 GGATTCAG 9

RESULT 15
US-09-851-062-23/c
Sequence 23; Application US/09851062
Accession No. US090851062.1
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
INVENTOR: Susan M. Freder
ATTORNEY: ANTHONY J. SHERMAN
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
FILE REFERENCE: RTS-0247
CURRENT APPLICATION NUMBER: US/09/851,062
CURRENT FILING DATE: 2001-05-07
SOFTWARE: Patent Ver. 2.1
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 29
LENGTH: 20
SEQUENCE:
GGATTCAG
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-23

Query Match
Accession No. US090851062.1 100.0%; Score 9; DB 4; Length 20;
Matched Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGATTCAG 9
1 GGATTCAG 11

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Search completed: January 1, 2004, 00:32:18
 Job time : 35.0856 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
ON nucleic - nucleic search, using sw model
Run on: December 31, 2003, 17:10:00, Search time 164.924 Seconds
296.996 Million cell updates/sec
(without alignment)

Title: US-09-540-843-1
Perfect score: 1 gattatgag 9
Sequence: 1 gattatgag 9
Scoring table: IDENTITY, NUC
Gapop 10.0, Gapext 1.0
Searched: 2263443 seqs, 1710637950 residues
Total number of hits satisfying chosen parameters: 998502
Minimum DB seq length: 30
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Lustig first 45 summaries
Database: Published Applications, MA*

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- 18: /cgn2_6/pdata1/pubma/US10E_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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	17	9	100.0	20	11	US-09-774-809-102
	18	9	100.0	20	11	US-10-128-870-15
	19	9	100.0	20	11	US-10-128-870-15
	20	9	100.0	20	11	US-10-128-870-15
c	21	9	100.0	20	15	US-10-047-511-32
	22	9	100.0	24	9	US-09-815-654-23
	23	9	100.0	25	9	US-09-866-108-5679
	24	9	100.0	25	9	US-09-866-108-5679
	25	9	100.0	25	9	US-09-866-108-5681
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	27	9	100.0	25	9	US-09-866-108-5683
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	31	9	100.0	25	9	US-09-866-108-5687
	32	9	100.0	25	9	US-09-866-108-5688
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	34	9	100.0	25	9	US-09-866-108-5690
	35	9	100.0	25	9	US-09-866-108-5691
	36	9	100.0	25	9	US-09-866-108-5692
	37	9	100.0	25	9	US-09-866-108-5693
	38	9	100.0	25	9	US-09-866-108-5694
	39	9	100.0	25	9	US-09-866-108-5695
	40	9	100.0	25	11	US-09-911-904-37
	41	9	100.0	25	15	US-10-215-112-4285
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	43	9	100.0	25	15	US-10-215-112-4285
c	44	9	100.0	25	15	US-10-215-112-10891
	45	9	100.0	25	15	US-10-098-2618-9340

ALIGNMENTS

RESULT 1
Sequence 1, Application US/1012630
GENERAL INFORMATION:
APPLICANT: Gluchrest, Barbara A.
APPLICANT: Yiller, Mark S.
TITLE OF INVENTION: Oligonucleotides
TITLE OF INVENTION: Algorithm to Inhibit Cell Growth Using
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/10/122,630
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/467,012
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: PCT/US01/10162
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1
SEQ ID NO: 2
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1

Query Match 100.0% Score 9, DB 15, Length 9,
Best Local Similarity 100.0% Pred No. 3 84+08
Matches 9; Conservative 0; Mismatch 0; Indels 0; Gaps 0;
1 GATTATGAG 9

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Db      1 GAGTATGAG 9

RESULT 2
US-10-150-779A-15/C Application US/1012633
Sequence 1, Application US/1012633
Publication No. US2003032611A1
GENERAL INFORMATION:
APPLICANT: MISSENBACH, MARGIT
APPLICANT: KUCH, TROELS
APPLICANT: ELLER, Mark S.
APPLICANT: YAR, Mima
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
Oligonucleotides
FILE REFERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US/10/122,433
PRIOR APPLICATION NUMBER: US/09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR PCT NUMBER: PCT/US03/10162
PRIOR FILING DATE: 2003-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQUENCE ID NOS: 15
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1
Query Match 100.0%; Score 9; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+08; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGTATGAG 9
Db      1 GAGTATGAG 9

RESULT 3
US-10-150-779A-15/C Application US/10150779A
Sequence 1, Application US/10150779A
Publication No. US20030325241A1
GENERAL INFORMATION:
APPLICANT: MISSENBACH, MARGIT
APPLICANT: KUCH, TROELS
APPLICANT: ORUM, HENRIK
APPLICANT: HANSEN, BO
TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
INFECTIOUS DISEASES
FILE REFERENCE: 55704 (45120)
CURRENT APPLICATION NUMBER: US/10/150,779A
PRIOR APPLICATION NUMBER: US/09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR PCT NUMBER: PCT/US03/10162
PRIOR FILING DATE: 2003-03-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Ver. 2.1
SEQUENCE ID NOS: 16
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
Oligonucleotide
US-10-150-779A-15
Query Match 100.0%; Score 9; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+08; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGTATGAG 9
Db      1 GAGTATGAG 4

RESULT 4
US-10-150-779A-15/C Application US/10150779A
Sequence 1, Application US/10150779A
Publication No. US20030325241A1
GENERAL INFORMATION:
APPLICANT: MISSENBACH, MARGIT
APPLICANT: KUCH, TROELS
APPLICANT: ORUM, HENRIK
APPLICANT: HANSEN, BO
TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
INFECTIOUS DISEASES
FILE REFERENCE: 55704 (45120)
CURRENT APPLICATION NUMBER: US/10/150,779A
PRIOR APPLICATION NUMBER: US/09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR PCT NUMBER: PCT/US03/10162
PRIOR FILING DATE: 2003-03-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq Ver. 2.1
SEQUENCE ID NOS: 16
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
Oligonucleotide with phosphorothioate backbone
US-10-150-779A-15
Query Match 100.0%; Score 9; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+08; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGTATGAG 9
Db      1 GAGTATGAG 4

RESULT 5
US-09-866-108-2750
Sequence 2750, Application US/09866108
Publication No. US2003032860A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yongshang
APPLICANT: HAN, YONG G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenhuang
APPLICANT: CHEN, Wenhuang
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR APPLICATION NUMBER: US/09/207,456
PRIOR FILING DATE: 2000-05-29
PRIOR PCT NUMBER: PCT/US01/06667
PRIOR FILING DATE: 2001-01-30
PRIOR PCT NUMBER: PCT/US01/06664
PRIOR FILING DATE: 2001-01-30
PRIOR PCT NUMBER: PCT/US01/06669
PRIOR FILING DATE: 2001-01-30
PRIOR PCT NUMBER: PCT/US01/06665
PRIOR FILING DATE: 2001-01-30
PRIOR PCT NUMBER: PCT/US01/06668
PRIOR FILING DATE: 2001-01-30

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1	PRIOR APPLICATION NUMBER: US 60/266,860	Query Match	100.0%	Score 9;
2	PRIOR FILING DATE: 2001-02-05	Sequence Similarity	100.0%	Score 9;
3	NUMBER OF SEQ IDS NOS: 15752	Match	1	Match
4	SEQUENCE: Homo sapiens	Match	9	Match
5	SEQ ID NO 2751	Match	9	Match
6	LENGTH: 17	Match	9	Match
7	TYPE: DNA	Match	9	Match
8	US-09-866-108-2751	Match	9	Match
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111		Match	9	Match
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113		Match	9	Match
114		Match		

US-09-866-108-2752

06 OCT 1968

PAGE 01

Db 5 GAGTATG 13

1 FOLIOLE NO. 03040200100000A
1 GENERAL INFORMATION:
1
1 APPLICANT: GU, Yizhong
1 APPLICANT: JI, Yonggang
1 APPLICANT: JI, Yonggang
1 APPLICANT: PENN, Sharon G.
1 APPLICANT: HANZEL, David K.
1 APPLICANT: RANK, David R.
1 APPLICANT: CHEN, Mensheng

Copied from 09980559 on 05/19/2004

1	PRIOR FILING DATE:	2000-09-27
2	PRIOR APPLICATION NUMBER:	PCT/US01/00666
3	PRIOR FILING DATE:	2000-01-30
4	PRIOR APPLICATION NUMBER:	PCT/US01/00667
5	PRIOR FILING DATE:	2000-01-30
6	PRIOR APPLICATION NUMBER:	PCT/US01/00668
7	PRIOR FILING DATE:	2001-01-30
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9	PRIOR FILING DATE:	2001-01-30
10	PRIOR APPLICATION NUMBER:	PCT/US01/00665
11	PRIOR FILING DATE:	2001-01-30
12	PRIOR APPLICATION NUMBER:	PCT/US01/00668
13	PRIOR FILING DATE:	2001-01-30
14	PRIOR APPLICATION NUMBER:	PCT/US01/00662
15	PRIOR FILING DATE:	2001-01-30
16	PRIOR APPLICATION NUMBER:	PCT/US01/00661
17	PRIOR FILING DATE:	2001-01-30
18	PRIOR APPLICATION NUMBER:	PCT/US01/00670
19	PRIOR FILING DATE:	2001-01-30
20	PRIOR APPLICATION NUMBER:	US 60/334,687
21	PRIOR FILING DATE:	1999-09-27
22	PRIOR APPLICATION NUMBER:	US 60/266,860
23	PRIOR FILING DATE:	2001-02-05
24	PRIOR APPLICATION NUMBER:	US 60/270,456
25	PRIOR FILING DATE:	1975-05-08
26	PRIOR APPLICATION NUMBER:	1575-05-08
27	SOFTWARE:	GenBank's annotated Eukaryotic Coding Sequence Listing Engine
28	SEQ ID NO 2756	
29	LENGTH:	17
30	ORGANISM:	Homo sapiens
31	OS=NM_004616.1	
32	OS=U9-866-108-2756	
33	QUANTITY:	100.00
34	BEST LOCAL SIMILARITY:	100.00; Pred. No.
35	MATCHES:	9; Conservative; 0; Mismatch
36	QY	1 GAGTGTATG 9
37	DB	3 GAGTGTATG 11
38	RESULT 12	
39	Sequence 2756 Application US/09866108	
40	US-U9-866-108-2757	
41	GENERAL INFORMATION:	SEQUENCE INFORMATION
42	APPLICANT:	Gf, Yizhong
43	INVENTOR:	KENN, Stephen G.
44	APPLICANT:	KENNEL, David K.
45	APPLICANT:	RANK, David R.
46	APPLICANT:	SHANNON, Kenneth
47	FILE OF INVENTION:	MYOGEN-LIKE GENE EXPRES
48	TITLE REFERENCE:	ABMICA-7 US 09/866,108
49	CURRENT FILING DATE:	2001-05-25
50	PRIOR APPLICATION NUMBER:	US 60/236,359
51	PRIOR FILING DATE:	2000-05-26
52	PRIOR APPLICATION NUMBER:	US 60/236,359
53	PRIOR FILING DATE:	2000-10-04
54	PRIOR APPLICATION NUMBER:	US 60/236,359
55	PRIOR FILING DATE:	2000-09-27
56	PRIOR APPLICATION NUMBER:	PCT/US01/00666
57	PRIOR FILING DATE:	2001-01-30
58	PRIOR APPLICATION NUMBER:	PCT/US01/00667
59	PRIOR FILING DATE:	2001-01-30
60	PRIOR APPLICATION NUMBER:	PCT/US01/00664
61	PRIOR FILING DATE:	2001-01-30
62	PRIOR APPLICATION NUMBER:	PCT/US01/00669
63	PRIOR FILING DATE:	2001-01-30
64	PRIOR APPLICATION NUMBER:	PCT/US01/00665

REQUEST 15
 US-10-005-309-181
 Sequence 181, Application US/10205309
 GENERAL INFORMATION: 000100695A
 APPLICANT: Ribocigen Pharmaceuticals, Inc.
 APPLICANT: Ribocigen, James Neuroscience Medi-
 cal, Inc.
 TITLE OF INVENTION: Interfering RNA
 FILE OF REFERENCE: 900/033
 CURRENT APPLICATION NUMBER: US/10205309
 PUBLICATION NUMBER: 2010/00695A
 NUMBER OF SEQ NOS: 20
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 181
 LENGTH: 19
 ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sina sense
US-10-205-309-181
Query Match 100.0%; Score 9; DA 13; Length 19;
Best Local Similarity 77.8%; Pred. No. 1/7e04;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 GAGTATGAG 9
|||:||||
DB 9 GAGGAUGAG 17
Search completed: January 1, 2004, 01:10:34
Job time : 105.924 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Inc.

OW nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21, Search time 89.57 Seconds
 444.364 Million cell updates/sec
 (without alignment)

Title: US-09-540-843-2

Perfect score: 9

Sequence: 1 tagseqgat g

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 288871 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: gp-hum.*

2: gp-hum.*

3: gp-in.*

4: gp-in.*

5: gp-ov.*

6: gp-pat.*

7: gp-ph.*

8: gp-ph.*

9: gp-ph.*

10: gp-ro.*

11: gp-est.*

12: gp-est.*

13: gp-un.*

14: gp-vi.*

15: en-hum.*

16: en-hum.*

17: en-hum.*

18: en-in.*

19: en-in.*

20: en-ov.*

21: en-ov.*

22: en-ov.*

23: en-ph.*

24: en-ph.*

25: en-pl.*

26: en-ro.*

27: en-ro.*

28: en-un.*

29: en-vi.*

30: en-hg-hum.*

31: en-hg-hum.*

32: en-hg-Other.*

33: en-hg-mus.*

34: en-hg-mus.*

35: en-hg-ph.*

36: en-hg-ph.*

37: en-hg-vit.*

38: en-hg-vit.*

39: en-hgo-hum.*

40: en-hgo-mus.*

41: en-hgo-Other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	9	100.0	9	6	AX268754 Sequence
2	9	100.0	16	6	AX149832 Sequence
3	9	100.0	17	6	AX673343 Sequence
4	9	100.0	17	6	AX710036 Sequence
5	9	100.0	17	6	AX710036 Sequence
6	9	100.0	17	6	AX711799 Sequence
7	9	100.0	17	6	AX712235 Sequence
8	9	100.0	17	6	AX712235 Sequence
9	9	100.0	17	6	AX718033 Sequence
10	9	100.0	20	6	AX395111 Sequence
11	9	100.0	20	6	AX146956 Sequence
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16	9	100.0	21	6	AX288850 Sequence
17	9	100.0	22	6	E25148 Method for
18	9	100.0	23	6	E36547 Method of
19	9	100.0	23	6	E36547 Method of
20	9	100.0	23	11	DOC009056A
21	9	100.0	24	6	AR115197 Sequence
22	9	100.0	24	6	AR146693 Sequence
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27	9	100.0	26	6	AX526487 Sequence
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29	9	100.0	27	6	AX550552 Sequence
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31	9	100.0	27	6	AX550552 Sequence
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35	9	100.0	30	6	AX268754 Sequence
36	9	100.0	30	6	BD137726 Protein e
37	8	88.9	10	6	AX68162 Sequence
38	8	88.9	11	6	AX68162 Sequence
39	8	88.9	11	6	AX68162 Sequence
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42	8	88.9	15	6	AR033402 Sequence
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ALIGNMENTS

RESULT 1	AX268754	AX268754	8 bp	DNA
DEFINITION	Sequence 2 from Patent WO0174142.			
ACCESSION	AX268754.1	GI:16541826		
VERSION	AX268754.1			
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	artificial sequence.			
REFERENCE	Gichrest, B.A., Year, M. and Ellor, M.			
AUTHORS	Use of locally applied data fragments			
TITLE	Patent WO 0174142-A2 11-OCT-2001			
JOURNAL	JOURNAL			
	INSTRUMENTS OF BOSTON UNIVERSITY (US)			

linear PAT 29-OCT-2001

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FEATURES             Location/Qualifiers
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                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches              9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
Db 1 TAGGAGGAT 9
RESULT 2
LOCUS AX149832/c
DEFINITION Sequence 169 from Patent WO0198537.
ACCESSION AX149832
VERSION AX14982.1 GI:21524199
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Artificial sequences.
AUTHORS Lyamichev V., Allawi H., Dong F., Neri B.P. and Vener I.T.
CITILE Nucleic acid accessible hybridization sites
CITILE Third Wave Technologies, Inc. (US)
CITILE Third Wave Technologies, Inc. (US)
JOURNAL Location/Qualifiers
FEATURES             source
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Matches              9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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12 TAGGAGGAT 4
RESULT 3
LOCUS AX673343/c
DEFINITION Sequence 1788 from Patent WO0304526.
ACCESSION AX673343
VERSION AX673343.1 GI:29311691
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1. 17
AUTHORS Teleman A., Anson R. and Tuijinder M.
CITILE Sequences involved in phenomena of tumour suppression, tumour
CITILE regression, apoptosis and/or resistance to viruses and their use as
CITILE Patent: WO 0304526-A 1788 16-JUN-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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                        /mol_type="genomic DNA"
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BASE COUNT           2 a 4 c 4 g 7 t
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Best Local Similarity 100.0%; Pred. No. 1.8e+09;
Matches              9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
Db 1 TAGGAGGAT 2
RESULT 4
LOCUS AX727498/c
DEFINITION Sequence 5185 from Patent WO03023176.
ACCESSION AX727498
VERSION AX727498.1 GI:30506841
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
REFERENCE 1. 17
AUTHORS Teleman A., Anson R. and Tuijinder M.
CITILE Sequences involved in phenomena of tumour suppression, tumour
CITILE regression, apoptosis and/or virus resistance and their use as
CITILE Patent: WO 03025176-A 5185 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
                        source
                        1. 17
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:10090"
BASE COUNT           5 a 7 c 1 g 4 t
ORIGIN
Query Match          100.0%; Score 9; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+09;
Matches              9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
Db 1 TAGGAGGAT 2
RESULT 5
LOCUS AX730036/c
DEFINITION Sequence 1670 from Patent WO03023175.
ACCESSION AX730036
VERSION AX730036.1 GI:30509379
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1. 17
AUTHORS Teleman A., Anson R. and Tuijinder M.
CITILE Sequences involved in phenomena of tumour suppression, tumour
CITILE regression, apoptosis and/or virus resistance and their use as
CITILE Patent: WO 03025175-A 1670 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
                        source
                        1. 17
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                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
BASE COUNT           6 a 4 c 3 g 4 t
ORIGIN

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Query Match		100.0%; Score 9; DB 6; Length 17;	
Best Local Similarity		100.0%; Pred. No. 1.8e+05;	
Matches		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 TAGGAGAT 9		
Db	10 TAGGAGAT 2		
RESULT 6			
LOCUS	AX731799/c	Sequence 3433 from Patent WO03025175.	linear PAT 08-MAY-2003
DEFINITION	AX731799	17 bp DNA	
ACCESSION	AX731799.1	GI:3051142	
KEYWORDS	AX731799.1	GI:3051142	
SOURCE	AX731799.1	GI:3051142	
ORGANISM	AX731799.1	GI:3051142	
REFERENCE	AX731799.1	GI:3051142	
AUTHORS	AX731799.1	GI:3051142	
TITLE	AX731799.1	GI:3051142	
JOURNAL	AX731799.1	GI:3051142	
FEATURES	AX731799.1	GI:3051142	
BASE COUNT	AX731799.1	GI:3051142	
ORIGIN	AX731799.1	GI:3051142	
Query Match			
Best Local Similarity			
Matches			
Qy	1 TAGGAGAT 9		
Db	10 TAGGAGAT 2		
RESULT 7			
LOCUS	AX732013/c	Sequence 3623 from Patent WO03025177.	linear PAT 08-MAY-2003
DEFINITION	AX732013	17 bp DNA	
ACCESSION	AX732013.1	GI:305117321	
KEYWORDS	AX732013.1	GI:305117321	
SOURCE	AX732013.1	GI:305117321	
ORGANISM	AX732013.1	GI:305117321	
REFERENCE	AX732013.1	GI:305117321	
AUTHORS	AX732013.1	GI:305117321	
TITLE	AX732013.1	GI:305117321	
JOURNAL	AX732013.1	GI:305117321	
FEATURES	AX732013.1	GI:305117321	
BASE COUNT	AX732013.1	GI:305117321	
ORIGIN	AX732013.1	GI:305117321	
Query Match			
Best Local Similarity			
Matches			
Qy	1 TAGGAGAT 9		
Db	10 TAGGAGAT 2		
RESULT 8			
LOCUS	AX734589/c	Sequence 179 from Patent WO03025177.	linear PAT 08-MAY-2003
DEFINITION	AX734589	17 bp DNA	
ACCESSION	AX734589.1	GI:30513866	
KEYWORDS	AX734589.1	GI:30513866	
SOURCE	AX734589.1	GI:30513866	
ORGANISM	AX734589.1	GI:30513866	
REFERENCE	AX734589.1	GI:30513866	
AUTHORS	AX734589.1	GI:30513866	
TITLE	AX734589.1	GI:30513866	
JOURNAL	AX734589.1	GI:30513866	
FEATURES	AX734589.1	GI:30513866	
BASE COUNT	AX734589.1	GI:30513866	
ORIGIN	AX734589.1	GI:30513866	
Query Match			
Best Local Similarity			
Matches			
Qy	1 TAGGAGAT 9		
Db	10 TAGGAGAT 2		

Copied from 09980559 on 03/19/2004

Search completed: December 31, 2003, 17:09:41
Job time : 831.57 sec

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AUTHORS      Keith T.
TITLE         Novel human gene relating to respiratory diseases, obesity, and
JOURNAL       Inflammatory bowel disease
Genome       Patent No. 017894-A 200 25 OCT-2001;
Genome       Genbank: U000001 (HUGO)
FEATURES     Genes: 1
              Location/Qualifiers
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                  /db_xref="taxon:32630"
                  /db_type="genomic DNA"
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BASE COUNT   2 a      8 c      4 g      6 t
ORIGIN
Query Match 100.0%; Score 9; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1 8a-05;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAGGAGCAT 9
|||||
19 TAGGAGCAT 11

AB069488      20 bp DNA linear SYN 31-MAY-2003
1361 synthetic construct DNA, forward primer for human STS sts-M7099 at
1361
ACCESSION     AB069488
VERSION       AB069488.1 GI:15130292
DEFINITION    synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     Chen Y.Z., Hayashi Y., Wu J.G., Tanaka E., Maekawa K.,
              Matsumoto N., Inazawa J., Hosoda F., Arai Y., Mitushima H.,
              Morishima A., Ohira M., Nakagawa A., Liu S., Honji M., Horii A.
              A BAC-based STS-content map spanning a 35-Mb region of human
              chromosome 1p35-p36
              JOURNAL Molecular Pathology; 2-1 Setiyemachi, Aoba-ku, Sendai,
              Miyagi 980-8577, Japan. E-mail: cc.tanaka@cc.tohoku.ac.jp.
              Tel:81-22-717-8042, Fax:81-22-717-8047
              Location/Qualifiers
                1..20   join="synthetic construct"
                  /db_xref="taxon:32630"
                  /db_type="genomic DNA"
BASE COUNT   3 a      9 c      2 g      6 t
ORIGIN
misc_feature
1361 sts-M7099 obtained from clones B61B17, B66A23, B26B112,
1361 B316H11, B26P17, B17B92, B166B12, Human BAC library
1361
BASE COUNT   3 a      9 c      2 g      6 t
ORIGIN
Query Match 100.0%; Score 9; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1 8a-05;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAGGAGCAT 9
|||||
20 TAGGAGCAT 12

```


The library can be used for producing chimeric nucleic acids. ACC41551 to ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid sequences given in the exemplification of the present invention.

The library can be used for navigation and position of the network.

to ACC4175A and APP40919 to APP41015, renouncing nuc'otide and im-

CC sequences given in the exemplification of the present invention.
XX
SO Sequence 10 BP: 3 A: 0 C: 5 G: 2 T: 0 other:

Query Match 100.0%; Score 9; DB 25; Length 10;

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Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 TAGGAGGAT 9

db 2 TAGGAGGAT 10

RESULT 4

ABH73149
ID ABH73149 standard; DNA; 12 BP.

XX
AC ABH73149;

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 273134 for detecting SNP TSC0003058.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
nucleic acid; cytosine methylation; cardiovascular; primary; epigenetic

central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX AC AB114652;
 XX AC 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 314625 for detecting SNP TSC026468.
 XX DE SNP; single nucleotide polymorphism; human; diagnosis; RNA; cancer; CNS;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX KW Homo sapiens.
 XX OS Homo sapiens.
 XX OS WO200177384-A2.
 XX EN 18-OCT-2001.
 XX FR 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2002; 2000DE-1039173.
 XX EP (EP1G-) EP1GONOMICS AG.
 XX OL Olek A. Piepenbrock C. Berlin K.
 XX WT; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status.
 XX Claim 1: SEQ ID 314625, 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
 XX ABOC0010-ABC95989, ABF00010-ABF99989, ABH00010-ABH99989 and ABK00010-ABK99989 represent the oligomers described in the invention.
 XX AB100010-AB182073 represent the oligomers described in the printed specification, but was obtained in electronic format from MIP0 at ftp.vipo.int/pub/published_pct_sequences.
 XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 other;
 XX Query Match 100.0%; Score 9; DB 23; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 2.9e+04;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 TAGAGGAGAT 9
 XX 4 TAGAGGAGAT 12
 XX Db
 XX RESULT 13
 XX AB116049
 XX ID AB116049 standard; DNA; 12 BP.
 XX AC AB138611;
 XX AC 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 314624 for detecting SNP TSC0040564.
 XX DE SNP; single nucleotide polymorphism; human; diagnosis; RNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX OS WO200177384-A2.
 XX EN 18-OCT-2001.
 XX FR 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2002; 2000DE-1019173.
 XX EP (EP1G-) EP1GONOMICS AG.
 XX OL Olek A. Piepenbrock C. Berlin K.
 XX WT; 2001-657177/75.

XX WO200177384-A2.
 XX EN 18-OCT-2001.
 XX FR 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2002; 2000DE-1019173.
 XX EP (EP1G-) EP1GONOMICS AG.
 XX OL Olek A. Piepenbrock C. Berlin K.
 XX WT; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status.
 XX Claim 1: SEQ ID 316022; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
 XX ABOC0010-ABC95989, ABF00010-ABF99989, ABH00010-ABH99989 and ABK00010-ABK99989 represent the oligomers described in the invention.
 XX AB100010-AB182073 represent the oligomers described in the printed specification, but was obtained in electronic format from MIP0 at ftp.vipo.int/pub/published_pct_sequences.
 XX Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 other;
 XX Query Match 100.0%; Score 9; DB 23; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 2.9e+04;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 TAGAGGAGAT 9
 XX 2 TAGAGGAGAT 10
 XX Db
 XX RESULT 13
 XX AB138611
 XX ID AB138611 standard; DNA; 12 BP.
 XX AC AB138611;
 XX AC 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 314624 for detecting SNP TSC0040564.
 XX DE SNP; single nucleotide polymorphism; human; diagnosis; RNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX OS WO200177384-A2.
 XX EN 18-OCT-2001.
 XX FR 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2002; 2000DE-1019173.
 XX EP (EP1G-) EP1GONOMICS AG.
 XX OL Olek A. Piepenbrock C. Berlin K.
 XX WT; 2001-657177/75.

Qy 1 TAGAGENT 9
DB 1 TAGAGENT 9

Search completed: December 31, 2003, 15:08:13
Job time : 261.089 secs


```

Email: dunn@genetics.utah.edu
Seq primer: CTTGTAAACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19
Location/Qualifiers
FEATURES
    source
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /db_xref="taxon:10090"
            /clone="U00C1M015780"
            /sex="Male"
            /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"/
            /clone_lib="Mouse 10kb plasmid U00C1M library"
            /note="Vector: pMD22; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated into the blunt ends of the genomic DNA. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The selected DNA was digested with a derivative of pMD22 (g14732114) (pA12972), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and the resulting construct was transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
    base count
        4 a 0 c 5 g 6 t
    origin
        88.94; Score 8; DB 28; Length 19;
        Best Local Similarity 100.0%; Prod No. 5.3e+05;
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    qy
        1 TAGGCGCA 8
        11 TAGGAGCA 8
    db
        2 AGGAGG 9
        20 AGGAGG 13
    result 2
        20 bp DNA linear GSS 03-OCT-2000
        1M0146P20R Mouse 10kb plasmid U00C1M library Mus musculus genomic
        clone U00C1M015780 F, genomic survey sequence.
    accession
        A2393773.1 G1:10508845
    version
        A2393773.1
    keywords
        Mus musculus (house mouse)
    organism
        Eukaryota; Metazoa; Chordata; Carnata; Vertebrata; Eucelostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
        1 (bases 1 to 20) Barber M., Bascom T., Duval B., Hamil C.,
        Dunn D., Aoyagi A., Barber M., Bascom T., Duval B., Hamil C.,
        M. Rose M., Rose R., Stokes R., Tingey A., von Niederhausern A.
        and Wright D., Meise R.,
    title
        Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
    journal
        Unpublished
    contact
        Robert B. Weiss
        University of Utah Genome Center
        Ram. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
        84112, USA
        Tel: 801 565 5606
    comment

```

[illegible]

PREFACE

Clone distribution. KCF-GAP clone distribution information can be
 found at: www.bio.lnln.gov/bbip/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gluco start: 0.00
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/clone="PM25174"

/tissue_type="adenoecarcinoma"

/lab_host="DH10B" cap frag.

/note="Organ: pancreas; vector: pGW-SORTS; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo df.

Average insert size 1.72 Kb. Life Technologies catalog #:

6 115154 9 C

5 g 2 t

BASE COUNT

ORIGIN

88.91; Score 8; DB 9; Length 22;

Best Local Similarity 100.0%; Pred. No. 6.2e+05; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGAGGAT 9

DB 9 AGAGGAT 2

1 TAGAGGA 8

12 TAGAGGA 19

1 TAGAGGA 19

1 TAGAGGA 19

1 TAGAGGA 19

1 TAGAGGA 19

1 TAGAGGA 19

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/seq="Wale"

/ab_bov="Coli strain X10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUCGM library"

/note="Vector: PM242v; Purified genomic DNA from M.

musculus C57BL/6J; Samples were obtained from the Jackson

Lab. M. Mus. DNA source: documents/dnars/). The DNA

was hydrodynamically sheared by repeated passage through a

20-gauge needle. The sheared DNA was ligated with DNA

polynucleotide kinase. Adapter oligonucleotides were

ligated to the blunt ends in high molar excess. The

ligation mixture was then digested with EcoRI for 4.5 to

10.5 bp range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PM242 gl1432114[gs AP128972.1], a copy-number ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA. The resulting UUCGM library was

sequenced using the primer Oligo df. The UUCGM library was

selected for ampicillin resistance."

2 a 8 5 g

3 a 8 5 g

4 a 8 5 g

5 a 8 5 g

6 a 8 5 g

7 a 8 5 g

8 a 8 5 g

9 a 8 5 g

10 a 8 5 g

11 a 8 5 g

12 a 8 5 g

13 a 8 5 g

14 a 8 5 g

15 a 8 5 g

16 a 8 5 g

17 a 8 5 g

18 a 8 5 g

19 a 8 5 g

20 a 8 5 g

21 a 8 5 g

22 a 8 5 g

23 a 8 5 g

24 a 8 5 g

25 a 8 5 g

26 a 8 5 g

27 a 8 5 g

28 a 8 5 g

29 a 8 5 g

30 a 8 5 g

31 a 8 5 g

32 a 8 5 g

33 a 8 5 g

34 a 8 5 g

35 a 8 5 g

36 a 8 5 g

37 a 8 5 g

38 a 8 5 g

39 a 8 5 g

40 a 8 5 g

41 a 8 5 g

42 a 8 5 g

43 a 8 5 g

44 a 8 5 g

45 a 8 5 g

46 a 8 5 g

47 a 8 5 g

48 a 8 5 g

49 a 8 5 g

50 a 8 5 g

51 a 8 5 g

52 a 8 5 g

53 a 8 5 g

54 a 8 5 g

55 a 8 5 g

56 a 8 5 g

57 a 8 5 g

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RESULT 12
A2495986 25 bp DNA linear GSS 05-OCT-2000
LOCUS
DEFINITION
A2495986 mouse 10kb plasmid UUCM3 library Mus musculus genomic
clone UUCM3033309 r, genomic survey sequence.

ACCESSION
A2495986.1 GI:10673556
VERSION
SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. Base 1 to 253

Dunn, D., Ayoubi, A., Barber, M., Becorn, T., Duval, B., Hail, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, F., Pedersen, T., Reilly,

and Wright, D., Stokes, R., Tingey, A., von Molthausen, A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Contact: Robert B. Weiss

University of Utah Genome Center

Room 108, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel.: 801 585 5606

Email: dummetts@genome.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0333 Row: H Column: 09

Clase: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/db_xref="GeneID:1033309"

/db_xref="Ensembl:UUCM3033309"

/taxe="Mammalia"

/clone_lib="house 10kb plasmid UUCM3 library from M.

/note="Vector: PM294inv; Purified genomic DNA from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

(http://www.jax.org/resources/documents/musres/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was ligated to a BamHI-digested pUC19 vector and transformed into

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range. The library was stored at -80°C in 100% ethanol.

electrophoresis. Vector DNA was prepared from a derivative

of pMD22 (GI:1473214) [9b] (pAR2907-1), a copy-number

plasmid vector. The library was ligated into the vector with

with adaptor components to the insert. The library was

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA and transformed into

competent cells (Stratagene). Cells were selected for

and selected for ampicillin resistance.

BASE COUNT 12 a 1 c 10 g 2 t

ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 25;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAGAGAGA 8

17 TAGAGAGA 24

17 TAGAGAGA 24

17 TAGAGAGA 24

17 TAGAGAGA 24

17 TAGAGAGA 24

17 TAGAGAGA 24

RESULT 13

B0592300/c

LOCUS

DEFINITION

B0592300/c

ACCESSION

B0592300.1

VERSION

B0592300.1

SOURCE

Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophytes; Equisetum; Gymnosperms; Angiosperms; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1. Base 1 to 278

Weisbecker, B., Hwang, S., Steinfach, M.,

Drungowski, M., Strahl, D., Mucke, A., Menze, A., O'Brien, J., Lebrach, H.,

and Radcliff, U.

Construction of a 'unigenic' cDNA clone set by oligonucleotide

screening of a cDNA library from 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2003)

Contact: Weisbecker, B.

ADIS DNA core facility at MPZ

Carl-von-Linné Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisbecker@mpz.uni-koeln.mpg.de

Plate: 21 Row: P Column: 06

Seq primer: SP6; CATACATTAGTCACTATAC.

Location/Qualifiers

/organism="Beta vulgaris"

/mol_type="mRNA"

/multiview="KMG220 (double haploid, monogerm breeding line

/db_xref="GABI:190689"

/db_xref="taxon:161934"

/db_xref="GeneID:1033309"

/db_xref="Ensembl:UUCM3033309"

/tissue_type="developing root"

/lab_host="EMDH08"

/clone_lib="MPZ cDNA library from 25,000 potential sugar beet genes"

/note="Site 2, NotI;

Kleinwiesener Saatzucht AG, Linbeck, Germany, contact:

orientations.de; cloning sites SalI-NotI, primer sites and

SP6-SalI-CCAGCGTCGCG-SalI-polyA-CC-NotI-77; Note:

sequencing granted in the context of the GABI-BT project

Christian Jung; Sequence submission managed by

REP0/GABI-Primary database: http://gabi.rtpd.de"

BASE COUNT 8 a 5 c 5 g 9 t

ORIGIN

Query Match 88.9%; Score 8; DB 13; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AGGAGAT 9

18 AGGAGAT 11

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18 AGGAGAT 11

RESULT 14

BH903668

LOCUS

DEFINITION

BH903668

ACCESSION

BH903668

VERSION

BH903668

SOURCE

Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophytes; Equisetum; Gymnosperms; Angiosperms; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1. Base 1 to 278

Weisbecker, B., Hwang, S., Steinfach, M.,

Drungowski, M., Strahl, D., Mucke, A., Menze, A., O'Brien, J., Lebrach, H.,

and Radcliff, U.

Construction of a 'unigenic' cDNA clone set by oligonucleotide

screening of a cDNA library from 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2003)

Contact: Weisbecker, B.

ADIS DNA core facility at MPZ

Carl-von-Linné Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisbecker@mpz.uni-koeln.mpg.de

Plate: 21 Row: P Column: 06

Seq primer: SP6; CATACATTAGTCACTATAC.

Location/Qualifiers

/organism="Beta vulgaris"

/mol_type="mRNA"

/multiview="KMG220 (double haploid, monogerm breeding line

/db_xref="GABI:190689"

/db_xref="taxon:161934"

/db_xref="GeneID:1033309"

/db_xref="Ensembl:UUCM3033309"

/tissue_type="developing root"

/lab_host="EMDH08"

/clone_lib="MPZ cDNA library from 25,000 potential sugar beet genes"

/note="Site 2, NotI;

Kleinwiesener Saatzucht AG, Linbeck, Germany, contact:

orientations.de; cloning sites SalI-NotI, primer sites and

SP6-SalI-CCAGCGTCGCG-SalI-polyA-CC-NotI-77; Note:

sequencing granted in the context of the GABI-BT project

Christian Jung; Sequence submission managed by

REP0/GABI-Primary database: http://gabi.rtpd.de"

BASE COUNT 8 a 5 c 5 g 9 t

ORIGIN

Query Match 88.9%; Score 8; DB 13; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AGGAGAT 9

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18 AGGAGAT 11

RESULT 15

BH903668

LOCUS

DEFINITION

BH903668

ACCESSION

BH903668

VERSION

BH903668

SOURCE

Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophytes; Equisetum; Gymnosperms; Angiosperms; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1. Base 1 to 278

Weisbecker, B., Hwang, S., Steinfach, M.,

Drungowski, M., Strahl, D., Mucke, A., Menze, A., O'Brien, J., Lebrach, H.,

and Radcliff, U.

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screening of a cDNA library from 25 000 potential sugar beet genes

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Carl-von-Linné Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisbecker@mpz.uni-koeln.mpg.de

Plate: 21 Row: P Column: 06

Seq primer: SP6; CATACATTAGTCACTATAC.

Location/Qualifiers

/organism="Beta vulgaris"

/mol_type="mRNA"

/multiview="KMG220 (double haploid, monogerm breeding line

/db_xref="GABI:190689"

/db_xref="taxon:161934"

/db_xref="GeneID:1033309"

/db_xref="Ensembl:UUCM3033309"

/tissue_type="developing root"

/lab_host="EMDH08"

/clone_lib="MPZ cDNA library from 25,000 potential sugar beet genes"

/note="Site 2, NotI;

Kleinwiesener Saatzucht AG, Linbeck, Germany, contact:

orientations.de; cloning sites SalI-NotI, primer sites and

SP6-SalI-CCAGCGTCGCG-SalI-polyA-CC-NotI-77; Note:

sequencing granted in the context of the GABI-BT project

Christian Jung; Sequence submission managed by

REP0/GABI-Primary database: http://gabi.rtpd.de"

BASE COUNT 8 a 5 c 5 g 9 t

ORIGIN

Query Match 88.9%; Score 8; DB 13; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 AGGAGAT 9

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FEATURES
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Location/Qualifiers
/corganism="Mus musculus"
/strain="C57BL/6J"
/db="xref:taxon:10090"
/cclone="MGC19032504"
/lab hosts="E. Coli strain XL1
/clote lib="Mouse 10kb strain
/note="Vector, 10kb, purified
from genomic DNA, 10kb, purified
Laboratory Mouse DNA Resource
High qual/Qualifiers

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was ligated with BamHI-digested pCMVcat and poly nucleotide kinase treated and adaptor oligonucleotides were ligated to the blunt ends in high molar excesses. The adaptor DNA was purified and size-selected for a 9.5 to 10 kb range by preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW2 [gib732114] (ATCC 29272), a copy-number inducible derivative of plasmid R1. The vector was ligated with BamHI-digested pCMVcat and adaptor oligonucleotides. The sheared, adaptor mouse DNA was annealed to the digested vector DNA and transformed into chemically-competent *E. coli* XL1-Gold (Stratagene) cells as described previously [Sambrook et al., 1989].

4 6 7 8 9 10 11 12
a b c d e f g h i

```

Query Match      89.9% ; Score 8 ; DB 28 ; Length 28 ;
Best local Similarity 100.0% ; Prod. No. 6.6e+05 ;
Matches 8 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Oy      1 TAGGAGCA 8
        |||||
Db       13 TAGGAGCA 6

Search completed: December 31, 2003, 19:41:13
Job time : 1038.09 secs

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ps 0;


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Db      1 TAGGAGGT 9
      |||||
      1 TAGGAGGT 9

RESULT 2
US-10-122-633-2
; Sequence 2, Application US/10122633
; Publication No. US2003032611A1
; GENERAL INFORMATION:
; APPLICANT: Glitcher, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054-1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR APPLICATION NUMBER: US 59/540,843
; PRIOR FILING DATE: 2000-03-31
; PUBLICATION DATE: 2003-07-09/01/0162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-2
Query Match      100.0%; Score 9; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+08;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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      |||||
1 TAGGAGGT 9

RESULT 3
US-10-223-765-202
; Sequence 3, Application US/1023765
; Publication No. US2003016597A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Sook
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Yoo, Myung-Sun
; APPLICANT: Kim, Myung-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PUBLICATION DATE: 2003-01-13/11,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 102
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
US-10-223-765-202
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Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db      1 TAGGAGGT 9
      |||||
      1 TAGGAGGT 9

RESULT 4
US-09-882-945A-169/c
; Sequence 169, Application US/09882945A
; Publication No. US2003014353A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichov, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Lyamichov, Victor
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: 0054-1088-019
; CURRENT APPLICATION NUMBER: US/09/882,945A
; PRIOR APPLICATION NUMBER: US 59/540,843
; PRIOR FILING DATE: 2001-06-15
; PUBLICATION DATE: 2003-07-09/01/0162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 169
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-169
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Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 TAGGAGGT 9
      |||||
      1 TAGGAGGT 9

RESULT 5
US-10-340-192-32/c
; Sequence 22, Application US/10340192
; Publication No. US20030170700A1
; GENERAL INFORMATION:
; APPLICANT: Lyng Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin A
; APPLICANT: Goss, David
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: 37-00061005
; CURRENT FILING DATE: 2003-01-08
; CURRENT APPLICATION NUMBER: US/10/340,192
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 12
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-340-192-32
Query Match      100.0%; Score 9; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 TAGGAGGT 9
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RESULT 6
US-10-339-793-97/c
; Sequence 97, Application US/10339793
; Publication No. US2003018076A1
; GENERAL INFORMATION:

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RESULT 11
US-10-066-191-104
  FILE REFERENCE: 20463-008
  CURRENT APPLICATION NUMBER: US/10/066,191
  PRIOR APPLICATION NUMBER: US/10/066,191
  PUBLICATION NO: US2003014422A1
  GENERAL INFORMATION:
  APPLICANT: William Gaarde
  TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
  FILE REFERENCE: RTS-0274
  CURRENT APPLICATION NUMBER: US/10/066,191
  PRIOR APPLICATION NUMBER: US/10/066,191
  NUMBER OF SEQ ID NOS: 153
  SEQ ID NO 104
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE: INFORMATION: Antisense Oligonucleotide
  OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
  US-10-066-191-104
  Query Match 100.0% Score 9; DB 13; Length 20;
  Best Local Similarity 100.0% Pred. No. 3.6e+04;
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  DB 7 TAGAGGAT 15

RESULT 12
US-09-816-814-13/c
  FILE REFERENCE: 20463-008
  CURRENT APPLICATION NUMBER: US/09/816,814
  PRIOR APPLICATION NUMBER: US/09/816,814
  PUBLICATION NO: US2003027136A1
  GENERAL INFORMATION:
  APPLICANT: Wayne, Cornelia M.
  TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THERO
  FILE REFERENCE: 07019-251001
  CURRENT APPLICATION NUMBER: US/09/816,814
  PRIOR APPLICATION NUMBER: US/09/816,814
  NUMBER OF SEQ ID NOS: 23
  SEQ ID NO 13
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE: INFORMATION: primer for PCR
  OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
  US-09-816-814-13/c
  Query Match 100.0% Score 9; DB 11; Length 21;
  Best Local Similarity 100.0% Pred. No. 3.6e+04;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TAGAGGAT 9
  DB 15 TAGAGGAT 7

RESULT 13
US-10-160-764-17
  FILE REFERENCE: 20463-008
  CURRENT APPLICATION NUMBER: US/10/160,764
  PRIOR APPLICATION NUMBER: US/10/160,764
  PUBLICATION NO: US2003018932A1
  GENERAL INFORMATION:
  APPLICANT: Huang, Yafan
  TITLE OF INVENTION: IDENTIFICATION AND MAPPING OF SINGLE NUCLEOTIDE
  FILE REFERENCE: 2001-04-30
  CURRENT APPLICATION NUMBER: US/10/160,764
  PRIOR APPLICATION NUMBER: US/10/160,764
  NUMBER OF SEQ ID NOS: 90
  SEQ ID NO 17
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE: INFORMATION: Identification and Mapping of Single Nucleotide
  OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
  US-10-160-764-17
  Query Match 100.0% Score 9; DB 13; Length 21;
  Best Local Similarity 100.0% Pred. No. 3.6e+04;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TAGAGGAT 9
  DB 17 TAGAGGAT 9

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RESULT 14
US-10-098-341/c
  FILE REFERENCE: 20463-008
  CURRENT APPLICATION NUMBER: US/10/098,341
  PRIOR APPLICATION NUMBER: US/10/098,341
  PUBLICATION NO: US2003018932A1
  GENERAL INFORMATION:
  APPLICANT: Alan
  TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THERO
  FILE REFERENCE: 2002-06-06
  CURRENT APPLICATION NUMBER: US/10/098,341
  PRIOR APPLICATION NUMBER: US/10/098,341
  NUMBER OF SEQ ID NOS: 352
  SEQ ID NO 341
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE: INFORMATION: primer
  OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
  US-10-098-341/c
  Query Match 100.0% Score 9; DB 13; Length 21;
  Best Local Similarity 100.0% Pred. No. 3.6e+04;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TAGAGGAT 9
  DB 17 TAGAGGAT 9

RESULT 15
US-10-037-632-48219/c
  FILE REFERENCE: 20463-008
  CURRENT APPLICATION NUMBER: US/10/037,632
  PRIOR APPLICATION NUMBER: US/10/037,632
  PUBLICATION NO: US20030204075A9
  GENERAL INFORMATION:
  APPLICANT: Wang, David G.
  TITLE OF INVENTION: IDENTIFICATION AND MAPPING OF SINGLE NUCLEOTIDE
  FILE REFERENCE: 2002-04-30
  CURRENT APPLICATION NUMBER: US/10/037,632
  PRIOR APPLICATION NUMBER: US/10/037,632
  NUMBER OF SEQ ID NOS: 9
  SEQ ID NO 9
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE: INFORMATION: Identification and Mapping of Single Nucleotide
  OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
  US-10-037-632-48219/c
  Query Match 100.0% Score 9; DB 13; Length 21;
  Best Local Similarity 100.0% Pred. No. 3.6e+04;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TAGAGGAT 9
  DB 17 TAGAGGAT 9

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Copied from 09980559 on 05/19/2004

GenCore version 3.1.6

Copyright (c) 1993 - 2003 CompuGen Inc.

ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 614.443 Seconds
 444.364 Million cell updates/sec
 Title: US-09-540-843-3
 Sequence: 1 agtata 7
 Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapex 1.0

Searched: 288971 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0

Minimum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 45 summaries

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 41: en-ba-hum*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	6	AZ68755 Sequence
2	7	100.0	7	6	AZ68755 Sequence
3	7	100.0	9	6	AZ68753 Sequence
4	7	100.0	10	6	AZ68753 Sequence
5	7	100.0	10	6	AZ68753 Sequence
6	7	100.0	10	6	AZ68753 Sequence
7	7	100.0	10	6	AZ68753 Sequence
8	7	100.0	10	6	AZ68753 Sequence
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10	7	100.0	10	6	AZ68753 Sequence
11	7	100.0	10	6	AZ68753 Sequence
12	7	100.0	10	6	AZ68753 Sequence
13	7	100.0	10	6	AZ68753 Sequence
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ALIGNMENTS

RESULT 1
 LOCUS US-09-540-843-3
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 VERSION
 SOURCE
 ORGANISM
 REFERENCES
 AUTHORS
 TITLE
 Patent: WO 01/442-A 3 11-OCT-2001;
 THUSTES OF ROSTON UNIVERSITY (US)

linear PAT 29-OCT-2001


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RESULT 14
LOCUS             AK626780                11 bp    DNA        linear    PAT 21-FEB-2003
DEFINITION        Sequence 3821 from Patent WO02053774.
ACCESSION         AK626780
VERSION           AK626780.1    GI:28454818
KEYWORDS
SOURCE
ORGANISM          Homo sapiens (human)
REFERENCE
  1. Petersohn, D., Conrath, M. and Hofmann, K.
    Method for determining homeostasis of the skin
    Patent: WO 02053774-A 3821 11-JUL-2002;
    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
BASE COUNT        5 a 4 0 c 3 g 3 t
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Query Match      100.0%; Score 7; DP 6; Length 11;
Best Local Similarity 100.0%; Proc No. 9 9+05;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ACTATGCA 7
|||||||
4 ACTATGCA 10

RESULT 15
LOCUS             AK629189                11 bp    DNA        linear    PAT 21-FEB-2003
DEFINITION        Sequence 6230 from Patent WO02053774.
ACCESSION         AK629189
VERSION           AK629189.1    GI:28457227
KEYWORDS
SOURCE
ORGANISM          Homo sapiens (human)
REFERENCE
  1. Petersohn, D., Conrath, M. and Hofmann, K.
    Method for determining homeostasis of the skin
    Patent: WO 02053774-A 6230 11-JUL-2002;
    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
BASE COUNT        4 a 3 c 1 g 3 t
ORIGIN
Query Match      100.0%; Score 7; DP 6; Length 11;
Best Local Similarity 100.0%; Proc No. 9 9+05;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ACTATGCA 7
|||||||
10 ACTATGCA 4

Search completed: December 31, 2003, 17:09:43
Job time : 646.543 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21, Search time 202.391 Seconds
(without initialisation)
93.410 Million cell updates/sec

Title: US-09-540-843-3

Sequence: 1 agatga 7

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

252756 seqs, 1349719017 residues

Local number of hits satisfying chosen parameters: 2101872

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing files: 15 summaries

Database:

1. N_Genescq-130und31.*
2. /SID81/Gcgdata/Genescq-emb1/NA1989.DAT.*
3. /SID81/Gcgdata/Genescq-emb1/NA1981.DAT.*
4. /SID81/Gcgdata/Genescq-emb1/NA1982.DAT.*
5. /SID81/Gcgdata/Genescq-emb1/NA1983.DAT.*
6. /SID81/Gcgdata/Genescq-emb1/NA1984.DAT.*
7. /SID81/Gcgdata/Genescq-emb1/NA1985.DAT.*
8. /SID81/Gcgdata/Genescq-emb1/NA1986.DAT.*
9. /SID81/Gcgdata/Genescq-emb1/NA1987.DAT.*
10. /SID81/Gcgdata/Genescq-emb1/NA1988.DAT.*
11. /SID81/Gcgdata/Genescq-emb1/NA1989.DAT.*
12. /SID81/Gcgdata/Genescq-emb1/NA1990.DAT.*
13. /SID81/Gcgdata/Genescq-emb1/NA1991.DAT.*
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15. /SID81/Gcgdata/Genescq-emb1/NA1993.DAT.*
16. /SID81/Gcgdata/Genescq-emb1/NA1994.DAT.*
17. /SID81/Gcgdata/Genescq-emb1/NA1995.DAT.*
18. /SID81/Gcgdata/Genescq-emb1/NA1996.DAT.*
19. /SID81/Gcgdata/Genescq-emb1/NA1997.DAT.*
20. /SID81/Gcgdata/Genescq-emb1/NA1998.DAT.*
21. /SID81/Gcgdata/Genescq-emb1/NA1999.DAT.*
22. /SID81/Gcgdata/Genescq-emb1/NA2000.DAT.*
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24. /SID81/Gcgdata/Genescq-emb1/NA2002.DAT.*
25. /SID81/Gcgdata/Genescq-emb1/NA2003.DAT.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	20 AAS10694	Oligonucleotide seq
2	7	100.0	7	23 AAS14907	Melanogenesis aso
3	7	100.0	7	23 AAS14911	Melanogenesis aso
4	7	100.0	7	23 AAS14915	Melanogenesis aso
5	7	100.0	9	23 AAS14905	Melanogenesis aso
6	7	100.0	10	21 AAS27895	Human dendritic ce
7	100.0	10	21 AAS26425	Metastatic breast	
8	7	100.0	10	21 AAS03760	LPS activated huma

10	7	100.0	10 22 AAS0636	Yeast WDF gene SA
11	7	100.0	10 22 AAS1979	Yeast WDF gene SA
12	7	100.0	10 22 AAF40876	Yeast WDF gene SA
13	7	100.0	10 24 AAF41870	Probe #3 used to i
14	7	100.0	10 24 AAF41870	Probe #3 used to i
15	7	100.0	10 24 AAF41870	Probe #3 used to i
16	7	100.0	10 24 AAF41870	Probe #3 used to i
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18	7	100.0	10 24 AAF41870	Probe #3 used to i
19	7	100.0	10 24 AAF41870	Probe #3 used to i
20	7	100.0	10 24 AAF41870	Probe #3 used to i
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22	7	100.0	10 24 AAF41870	Probe #3 used to i
23	7	100.0	10 24 AAF41870	Probe #3 used to i
24	7	100.0	10 24 AAF41870	Probe #3 used to i
25	7	100.0	10 24 AAF41870	Probe #3 used to i
26	7	100.0	10 24 AAF41870	Probe #3 used to i
27	7	100.0	10 24 AAF41870	Probe #3 used to i
28	7	100.0	10 24 AAF41870	Probe #3 used to i
29	7	100.0	10 24 AAF41870	Probe #3 used to i
30	7	100.0	10 24 AAF41870	Probe #3 used to i
31	7	100.0	10 24 AAF41870	Probe #3 used to i
32	7	100.0	10 24 AAF41870	Probe #3 used to i
33	7	100.0	10 24 AAF41870	Probe #3 used to i
34	7	100.0	10 24 AAF41870	Probe #3 used to i
35	7	100.0	10 24 AAF41870	Probe #3 used to i
36	7	100.0	10 24 AAF41870	Probe #3 used to i
37	7	100.0	10 24 AAF41870	Probe #3 used to i
38	7	100.0	10 24 AAF41870	Probe #3 used to i
39	7	100.0	10 24 AAF41870	Probe #3 used to i
40	7	100.0	10 24 AAF41870	Probe #3 used to i
41	7	100.0	10 24 AAF41870	Probe #3 used to i
42	7	100.0	10 24 AAF41870	Probe #3 used to i
43	7	100.0	10 24 AAF41870	Probe #3 used to i
44	7	100.0	10 24 AAF41870	Probe #3 used to i
45	7	100.0	10 24 AAF41870	Probe #3 used to i

ALIGNMENTS

RESULT 1	AA210694	AA210694 standard; DNA, 7 BP.
10	AA210694	AA210694 standard; DNA, 7 BP.
11	AA210694	AA210694 standard; DNA, 7 BP.
12	AA210694	AA210694 standard; DNA, 7 BP.
13	AA210694	AA210694 standard; DNA, 7 BP.
14	AA210694	AA210694 standard; DNA, 7 BP.
15	AA210694	AA210694 standard; DNA, 7 BP.
16	AA210694	AA210694 standard; DNA, 7 BP.
17	AA210694	AA210694 standard; DNA, 7 BP.
18	AA210694	AA210694 standard; DNA, 7 BP.
19	AA210694	AA210694 standard; DNA, 7 BP.
20	AA210694	AA210694 standard; DNA, 7 BP.
21	AA210694	AA210694 standard; DNA, 7 BP.
22	AA210694	AA210694 standard; DNA, 7 BP.
23	AA210694	AA210694 standard; DNA, 7 BP.
24	AA210694	AA210694 standard; DNA, 7 BP.
25	AA210694	AA210694 standard; DNA, 7 BP.
26	AA210694	AA210694 standard; DNA, 7 BP.
27	AA210694	AA210694 standard; DNA, 7 BP.
28	AA210694	AA210694 standard; DNA, 7 BP.
29	AA210694	AA210694 standard; DNA, 7 BP.
30	AA210694	AA210694 standard; DNA, 7 BP.
31	AA210694	AA210694 standard; DNA, 7 BP.
32	AA210694	AA210694 standard; DNA, 7 BP.
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36	AA210694	AA210694 standard; DNA, 7 BP.
37	AA210694	AA210694 standard; DNA, 7 BP.
38	AA210694	AA210694 standard; DNA, 7 BP.
39	AA210694	AA210694 standard; DNA, 7 BP.
40	AA210694	AA210694 standard; DNA, 7 BP.
41	AA210694	AA210694 standard; DNA, 7 BP.
42	AA210694	AA210694 standard; DNA, 7 BP.
43	AA210694	AA210694 standard; DNA, 7 BP.
44	AA210694	AA210694 standard; DNA, 7 BP.
45	AA210694	AA210694 standard; DNA, 7 BP.

PS3 activity; UV mmetric; UV-irradiation; UV-induced dermatosis; atopic dermatitis; allergic rhinitis; conjunctivitis; photoging; skin cancer; ss. Synthetic. GB236157-A. 24-MAR-1999; 99GB-0006758. 13-OCT-1999. 26-MAR-1998; 98US-0048927. (UYBO-) UNIV OSTON. Gilchrist BA, Yeart M, Eller M; WPI; 1999-543520/46.

The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-neuritic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes or a protective response to later exposure to UVB. The invention also describes the use of the oligonucleotides as cancer or a tumour metastasis factor inhibitor. Probably they mimic products of a DNA damage, or processed DNA-damage intermediates, by inducing the p53

PR inhibiting proliferation of epinncial cells, useful e.g. for treating
 PR carcinoma, using specific oligonucleotides that mimic the effects of
 PR ultra-violet light -
 XX
 PS Claim 1; Page 38; 74pp: English.
 PS
 XX

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 XX non-metastatic breast tumour tissue; gene therapy; anticancer;
 XX anti-metastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 XX W0945628-A2.
 XX 23-DEC-1999.
 XX 19-JUN-1999; 99W0-US13647.
 XX 19-JUN-1998; 98US-0089853.
 XX 13-JUN-1998; 98US-0089997.
 XX 13-JUN-1998; 98US-0090040.
 XX 19-JUN-1998; 98US-0090041.
 XX 19-JUN-1998; 98US-0090043.
 XX (GENE) GENZYME CORP.
 XX (ROBE) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 XX WPI; 2000-06079/09.
 XX Isolated polynucleotides differentially expressed in metastatic
 XX and non-metastatic breast cancer cells, useful for diagnosis,
 XX prevention and treatment of cancer.
 XX Claim 1, Page 208; 219pp; English.
 XX AZ82067 to AZ83941 represent tags corresponding to distinct
 XX tumour tissue (i.e. are upregulated in metastatic breast
 XX tumour tissue (i.e. are upregulated in metastatic breast tumour cells)
 XX AZ823942 to AZ82677 represent tags corresponding to distinct transcripts
 XX that are preferentially transcribed in the primary or non-metastatic
 XX breast cells (i.e. are downregulated in metastatic breast tumour
 XX cells). These transcripts can be used for diagnosis, prognosis,
 XX monitoring and treatment of breast cancer, particularly where metastatic.
 XX compounds that modulate expression of the transcription factors
 XX reactions. Compounds that modulate expression of the transcription factors
 XX potentially useful for treatment of (metastatic) breast cancer, while
 XX promoters from the transcripts are used to direct expression, in selected
 XX sequences), particularly an antigen-encoding sequence for use in gene or
 XX cell-based vaccines. Polypeptides encoded by the transcripts are also
 XX useful in vaccines; for diagnosing breast cancer and for raising
 XX therapeutic agents. Host cells that produce the polypeptides can be used
 XX to expand and isolate populations of educated, antigen-specific immune
 XX effector cells, e.g. cytotoxic T lymphocytes, and these used for
 XX adoptive immunotherapy.
 XX Sequence 10 BP; 5 A; 0 C; 2 G; 2 T; 0 other;
 XX Query Match 100.0%; Score 7; DB 21; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AGATGTA 7
 DB 4 AGATGTA 10
 RESULT 8
 AC AAH32760
 XX AAH32760 standard; cDNA; 10 BP.
 AC AAH32760;
 XX 13-AUG-2001 (first entry)
 DT

XX LPS activated human monocytic expression gene cDNA tag SEQ.133.
 XX Human; LPS; lipopolysaccharide; monocytic expression gene; tag; EST;
 XX expressed sequence tag; diagnosis; human disease; treatment; ss.
 XX Homo sapiens.
 XX JF2001065993-A.
 XX 21-MAR-2001.
 XX 28-APR-2000; 2000JP-0131079.
 XX 08-JUL-1999; 99JP-0195103.
 XX (KAGA-) KAGAKU GUUTSU SHINKO JIGYODAN.
 XX WPI; 2001-304363/32.
 XX LPS activated human monocytic expression gene group
 XX Claim 10; Page 28; 52pp; Japanese.
 XX The present invention describes an lipopolysaccharide (LPS) activated
 XX human monocytic expression gene group consisting of the high-ranking 50
 XX genes of the highest expression among the genes expressed by human
 XX sequence of (AAH32628 to AAH32677) continuous to the base sequence
 XX 5'-CATG-3' nearest to the polyA region. The gene group is useful for the
 XX development of new means for the diagnosis and the treatment of various
 XX CC AAH32628 to AAH32943 represent specifically claimed LPS activated human
 XX monocytic expression gene cDNA tags from the present invention. AAH32944
 XX represents a sequence of the LPS activated monocytic expression gene group
 XX encoding AAH32628 to AAH32943, which are given in the amplification of the present
 XX invention.
 XX Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 other;
 XX Query Match 100.0%; Score 7; DB 22; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AGATGTA 7
 DB 1 AGATGTA 7
 RESULT 9
 AC AAH39316
 XX AAH39316 standard; DNA; 10 BP.
 XX AAH39316;
 XX 23-MAR-2001 (first entry)
 DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5675.
 XX Year; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
 XX linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 XX MO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000MO-US16223.
 XX 16-JUN-1999; 99US-033032.
 XX

(UTYO) UNIV JOHNS HOPKINS.
Velculeaux V., Vogelstein B., Kinzler K,
WPI / 2003-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis
of gene expression (SAGE) tags, useful for studying, monitoring and
affecting phases of the cell cycle

Example, Page 202; 419pp; English.

The present invention describes an isolated DNA molecule comprising a
NORF gene which encodes a protein having at least one amino acid sequence
previously assigned open reading frame; or nonannotated ORP genes
comprising a SAGE (serial analysis of gene expression) tag. Also
described are: (1) a method (M1) of using NORF genes to affect the cell
cycle; (2) a method (M2) of identifying candidate NORF genes by
selecting from a library of cDNAs those which have a sequence identity
at least 10% between any two phases of the cell cycle selected from log
phase, S phase and G2/M; (3) a method (M3) for screening candidate
antifungal drugs comprising: a) contacting a test substance with a
yeast strain expressing a NORF gene whose expression varies as in M1, where a test substance which modifies the
expression of the yeast gene is a candidate antifungal drug; (3) a method
for identifying human genes which encode proteins involved in cell cycle
regulation comprising: a) comparing the DNA sequence of each cDNA
as in M1; and (4) a method (M4) for identifying a candidate drug as a
candidate drug in yeast cells comprising contacting a yeast cell with a
candidate drug and monitoring expression in the yeast cell of at least
one NORF gene whose expression is affected by the class of drugs. The NORF
genes described herein may be used to identify candidate drugs which
affect the cell cycle. The methods may be used to identify candidate drugs which
affect the cell cycle and for identification of antifungal drugs of the
present invention. AAF3262 to AAF3267 represent linkers and PCR
primers used in the SAGE method, in the exemplification of the present
invention.

Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 other:
Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Prod No. 5.7e+04; Matches 0; Gaps
Matches 0; Conservative 0; Mismatches 0; Indels 0

1 AGCTATGA 7
2 AGTATAA 8
|||||||
|||||||

RESULT 10
AAAF39793
ID AAF39793 standard; DNA; 10 BP.
AC AAF39793;
CC
TT
GG
AA 23-MAR-2001 (first entry)
DT
DE Yeast, Saccharomyces cerevisiae; Characterization; cell cycle; NORF;
KW Yeast, Saccharomyces cerevisiae; Characterization; cell cycle; NORF;
KW Serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WC0200077214-A2.
XX 21-DSC-2000
XX

Email: dunn@genetics.utah.edu
 Phone: 801 585 7177
 Fax: 801 585 7177
 Plates: 0086 row: E column: 14
 Seq primer: CACACGAGACACCTATGACC
 High quality sequence stop: 19
 Location/Qualifiers
 1..19

FEATURES

Source
 /organism="Mus musculus"
 /clone="UUCG10622010 P, genomic survey sequence."
 /db_xref="taxon:10090"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clove="C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was blunt end-ligated with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was ligated with a derivative of pMD18 (G14732114) (BART2002.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and the adapter DNA was purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 Query Match 100.0% Score 7; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AGTATCA 7
 |||||
 10 AGTATCA 16

RESULT 2
 A223945/c
 DEFINITION
 Clone UUCG10622010 P, genomic survey sequence.
 ACCESSION
 A223945
 VERSION
 A223945.1
 KEYWORDS
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 19)
 Dunn, D., Ayres, A., Barber, M., Bascorn, T., Duval, B., Hamil, C.,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., 2003. A whole genome scaffolding with paired end reads from 100k
 plasmid insects
 Unpublished
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 565 5606

Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /clone="UUCG10622010 P, genomic survey sequence."
 /db_xref="taxon:10090"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clove="C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was blunt end-ligated with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was ligated with a derivative of pMD18 (G14732114) (BART2002.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and the adapter DNA was purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

Source
 /organism="Mus musculus"
 /clone="UUCG10622010 P, genomic survey sequence."
 /db_xref="taxon:10090"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clove="C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was blunt end-ligated with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was ligated with a derivative of pMD18 (G14732114) (BART2002.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and the adapter DNA was purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 Query Match 100.0% Score 7; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AGTATCA 7
 |||||
 10 AGTATCA 16

RESULT 3
 A223945/c
 DEFINITION
 Clone UUCG10622010 P, genomic survey sequence.
 ACCESSION
 A223945
 VERSION
 A223945.1
 KEYWORDS
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 22)
 Dunn, D., Ayres, A., Barber, M., Bascorn, T., Duval, B., Hamil, C.,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., 2003. A whole genome scaffolding with paired end reads from 100k
 plasmid insects
 Unpublished
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Plasmid length: 10000 Gcd error: 0.00
 Seq primer: CTTGTAAAGCGCCGACGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

1..22
 /organism="Mus musculus"
 /clone="10b plasmid UGCGM library"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0462J10"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

The DNA was prepared by standard methods using a blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt end of the DNA. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The adaptor DNA was ligated with an inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to the adaptor DNA. The adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

7 a 5 c 2 g 8 t

Query Match 100.00; Score 7; DB 28; Length 22;

Similarity 100.00; Positives 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

11 AGTATGA 5

RESULT 4

DEFINITION 22 bp DNA linear GSS 14-DEC-2000
 Cloned into UGCGM03417, a genomic survey sequence.

Accession A268158.1 GI:11795304

Version A268158.1

Source Mus musculus (house mouse)

Organism Mus musculus

Reference Eukaryotes; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; 1 (base 1 to 22)

Authors Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, and Wright, D. Weiss, R.

Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Journal J. Biol. Chem. 275(18):13000-13005, 2000

Comment Contact: Robert B. Weiss
 University of Utah
 300, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Plasmid length: 10000 Gcd error: 0.00
 Seq primer: CACACGAGAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

1..22
 /organism="Mus musculus"
 /clone="10b plasmid UGCGM library"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM03417"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

The DNA was prepared by standard methods using a blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt end of the DNA. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The adaptor DNA was ligated with an inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to the adaptor DNA. The adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 0 c 9 g 7 t

Query Match 100.00; Score 7; DB 28; Length 22;

Similarity 100.00; Positives 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

4 AGTATGA 10

RESULT 5

DEFINITION 24 bp mRNA linear EST 23-AUG-2000
 Cloned into UGCGM03417, a genomic survey sequence.

Accession AM058679.1 GI:6652001

Version AM058679.1

Source Homo sapiens (human)

Organism Homo sapiens

Reference Eukaryotes; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; 1 (base 1 to 24)

Authors Brenner, S., Williams, S.R., Vernars, E.H., Storck, T., Moon, K., McCallum, C., Mao, J.J., Kitchner, J.J., Bleier, S., Durrig, R.B., and Wright, D. Weiss, R.

Title In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNA

Proc. Natl. Acad. Sci. USA 97 (4): 1665-1670 (2000)

Journal Proc. Natl. Acad. Sci. USA

Comment Contact: Burchan TS
 LYNN Therapeutics, Inc.
 2381 Industrial Blvd., Hayward, CA 94545, USA

Copied from 09980559 on 05/19/2004

	0.005 inch office at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were phosphorylated at their 5' ends. The adaptor DNA and sheared adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pUC18 by restriction enzyme digestion with EcoRI and ligated with an inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to the adaptor and ligated to form a recombinant construct. A chemically-competent E. coli XL10-Gold (Stratagene) cells were transformed with the recombinant construct and selected for ampicillin resistance."
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Local Similarity	100.0%; Score 7; DB 28; Length 25;
Matches	Conservative; 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 ACTATGA 7
Db	17 ACTATGA 11
RESULT 11	
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LOCUS	AZ802430 Mouse 10kb plasmid UGCM1 library Mus musculus genomic DNA linear GSS 16-FEB-2001
DEFINITION	UIGCMM0081122 P7, Genomic survey sequence.
ACCESSION	AZ802430.1 GI:12954813
VERSION	GSS mouse (house mouse)
FEATURES	musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rodentia; Rodentia; Sciurognathi; Muridae; Murine; Mus; Mus musculus
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Islam,H., Longcore,S., Mahmood,M., Meenen,G., Pedersen,T., Reilly and Wright D. Weiser, S., Stokes,R., Lingay,A., von Niederhausern,A., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Contact: Robert A. Neias
COMMENT	University of Utah Genome Center Department of Biology 84112 USA Commercial Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112 USA Fax: 801 585 5606 Email: dgonz@genome.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0061 row: 1 column: 22 Cloned Into: pUC18 Clase: plasmid end High quality sequence stop: 25. Location/Qualifiers /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J0090" /clone="UGCM0081122" /sex="Male"
FEATURES	/lab="Northwest Cell strain XH10-Gold TM resistant, F-" /notes="Vector: PMD2hy; Purified genomic DNA from M. musculus C57BL/6J (male); This sequence was obtained from the Jackson Laboratory Maine, Inc. Resources document at /diana/. The data was generated by the University of Utah Genome Center." ;

was bidirectionally clonamed by repeated passages through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt and repaired with T4 DNA polymerase and T4 polynucleotide kinase. Repaired oligonucleotides were ligated into BamHI-digested pUC19. The recombinant plasmid was adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The selected DNA was prepared from a derivative of pUC19 (p14732114) [98] BP23907. The vector was ligated with adaptor complementary to the insert, adaptor and adaptor vector DNA, and transformed into competent cells chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
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ORIGIN
Query Match 100.0%; Score 7; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQTGCA 7
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Db 22 AATGCA 16

RESULT 12
BMS52860
LOCUS
DEFINITION
BMS52860 48,55 x Arabidopsis thaliana TDNA insertion lines
survey sequence.

ACCESSION
BMS52860
VERSION
BMS52860.1
SOURCE
Arabidopsis thaliana

ORGANISM
Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R., Gadrinb J., Zimmermann J. and Ecker J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

COMMENT
Contact: Joseph R. Ecker
The Saik Institute for Biological Studies (SIGOAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 553 4100 x1752
Fax: 858 553 4100 x1752
Email: eckersa@saik.edu

FEATURES
This is a single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of AC3941627.

BASE COUNT
9 a 2 c 6 g 9 t

ORIGIN
Query Match 100.0%; Score 7; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQTGCA 7
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Db 22 AATGCA 16

RESULT 12
BMS52860
LOCUS
DEFINITION
BMS52860 48,55 x Arabidopsis thaliana TDNA insertion lines
survey sequence.

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQTGCA 7
|||||
Db 12 AATGCA 18

RESULT 13
BMS52860
LOCUS
DEFINITION
BMS52860 48,55 x Arabidopsis thaliana TDNA insertion lines
survey sequence.

ACCESSION
BMS52860
VERSION
BMS52860.1
SOURCE
Arabidopsis thaliana

ORGANISM
Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R., Gadrinb J., Zimmermann J. and Ecker J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

COMMENT
Contact: Joseph R. Ecker
The Saik Institute for Biological Studies (SIGOAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 553 4100 x1752
Fax: 858 553 4100 x1752
Email: eckersa@saik.edu

FEATURES
This is a single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of AC3941627.

BASE COUNT
9 a 2 c 6 g 9 t

ORIGIN
Query Match 100.0%; Score 7; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQTGCA 7
|||||
Db 12 AATGCA 18

RESULT 14
BMS57761/c
LOCUS
DEFINITION
BMS57761/c 49,95 x Arabidopsis thaliana TDNA insertion lines
survey sequence.

ACCESSION
BMS57761/c
VERSION
BMS57761/c.1
SOURCE
Arabidopsis thaliana

ORGANISM
Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R., Gadrinb J., Zimmermann J. and Ecker J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

COMMENT
Contact: Joseph R. Ecker
The Saik Institute for Biological Studies (SIGOAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 553 4100 x1752
Fax: 858 553 4100 x1752
Email: eckersa@saik.edu

FEATURES
This is a single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of AC3941627.

BASE COUNT
9 a 2 c 6 g 9 t

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Blasty sequence.
ACCESSION   BH857761.1 GI:21708582
VERSION    BH857761.1
KEYWORDS   GSS, ideopsis thaliana (thale cress)
SOURCE     Arabidopsis thaliana
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Taxonomy   Brassicaceae; Arabidopsia.
1 (bases 1 to 25)
REFERENCE   1 (bases 1 to 25)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
           ,C., Jesse,A., Kames,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
           et al.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL     Arabidopsis Genome
COMMENT    Unpublished
AUTHOR     Unpublished
JOURNAL    Saik Institute Genomic Analysis Laboratory (SIGAL)
           The Saik Institute for Biological Studies
           401 University Avenue, Suite 200, La Jolla, CA 92037, USA
           Tel: 858 453 1000 Fax: 858 453 1000
           Fax: 858 558 6379
Email: eckergsaik.edu
NOTES      The genomic sequence recovered from the left border of
           the T-DNA insertion site within an annotated intron of Atg52930.
           Class: T-DNA tagged.
FEATURES   source
            source
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /strain="Columbia 0"
            /clone="SAIK 015664.41.95.x"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /vector="pCambia" was performed on Arabidopsis thaliana lines
            of the T-DNA insertion lines. The T-DNA insertion lines
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the T-DNA insertion site. The T-DNA insertion site can
            be found at http://sigal.saik.edu/kdn\_protocols.html.
BASE COUNT  9 a 5 c 0 g 11 t
ORIGIN
Query Match 100.0%; Score 7; DB 28; Length 25;
Query Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTATGA 7
DB 8 AGTATGA 2

RESULT 15
LOCUS      26 bp DNA linear GSS 29-SEP-2000
DEFINITION clone UDCIM0080C6R Mouse 10kb plasmid UDCIM library Mus musculus genomic
ACCESSION   clone UDCIM0080C6R R, genomic survey sequence.
VERSION     A2345685.1 GI:10424922
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
           (bases 1 to 26)
AUTHORS     Duval,B., Barber,M., Beaumont,T., Duval,B., Hamil,C.,
           Islan,M., Longacre,S., Mahmoud,E., Meenen,E., Pedersen,T., Reilly
           M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
           et al.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL     Unpublished
COMMENT    Contact: Robert B. Weiss

```

```

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Phone: 801 585 5606
Fax: 801 585 7177
Email: ddunham@genetics.utah.edu
Insert Length: 10000 8cd error: 0.00
Insert Start: 10000 8cd error: 0.00
Seq Primer: CACACGGGAACGACCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
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            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /vector="pCambia" was performed on Arabidopsis thaliana lines
            of the T-DNA insertion lines. The T-DNA insertion lines
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the T-DNA insertion site. The T-DNA insertion site can
            be found at http://sigal.saik.edu/kdn\_protocols.html.
BASE COUNT  7 a 7 c 0 g 12 t
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Query Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTATGA 7
DB 9 AGTATGA 3

Search completed: December 31, 2003, 19:41:16
Job time : 807.231 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

ON nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21, Search time 469,316 Seconds
444,364 Million cell updates/sec

Title: US-09-540-843-4
Sequence: 1 gtagc 5

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Listing first 45 summaries

Genbank: 1
1: gb-hug.*
2: gb-hug.*
3: gb-hug.*
4: gb-hug.*
5: gb-hug.*
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41: gb-hug.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 2	5	100.0	5	6	AZ268756 Sequence
C 3	5	100.0	5	6	AZ268758 Sequence
C 4	5	100.0	5	6	AZ268755 Sequence
C 5	5	100.0	5	6	AZ268757 Sequence
C 6	5	100.0	5	6	AZ268759 Sequence
C 7	5	100.0	5	6	AZ268754 Sequence
C 8	5	100.0	5	6	AZ268753 Sequence
C 9	5	100.0	5	6	AZ268752 Sequence
C 10	5	100.0	5	6	AZ268751 Sequence
C 11	5	100.0	5	6	AZ268750 Sequence
C 12	5	100.0	5	6	AZ268749 Sequence
C 13	5	100.0	5	6	AZ268748 Sequence
C 14	5	100.0	5	6	AZ268747 Sequence
C 15	5	100.0	5	6	AZ268746 Sequence
C 16	5	100.0	5	6	AZ268745 Sequence
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C 19	5	100.0	5	6	AZ268742 Sequence
C 20	5	100.0	5	6	AZ268741 Sequence
C 21	5	100.0	5	6	AZ268740 Sequence
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C 24	5	100.0	5	6	AZ268737 Sequence
C 25	5	100.0	5	6	AZ268736 Sequence
C 26	5	100.0	5	6	AZ268735 Sequence
C 27	5	100.0	5	6	AZ268734 Sequence
C 28	5	100.0	5	6	AZ268733 Sequence
C 29	5	100.0	5	6	AZ268732 Sequence
C 30	5	100.0	5	6	AZ268731 Sequence
C 31	5	100.0	5	6	AZ268730 Sequence
C 32	5	100.0	5	6	AZ268729 Sequence
C 33	5	100.0	5	6	AZ268728 Sequence
C 34	5	100.0	5	6	AZ268727 Sequence
C 35	5	100.0	5	6	AZ268726 Sequence
C 36	5	100.0	5	6	AZ268725 Sequence
C 37	5	100.0	5	6	AZ268724 Sequence
C 38	5	100.0	5	6	AZ268723 Sequence
C 39	5	100.0	5	6	AZ268722 Sequence
C 40	5	100.0	5	6	AZ268721 Sequence
C 41	5	100.0	5	6	AZ268720 Sequence
C 42	5	100.0	5	6	AZ268719 Sequence
C 43	5	100.0	5	6	AZ268718 Sequence
C 44	5	100.0	5	6	AZ268717 Sequence
C 45	5	100.0	5	6	AZ268716 Sequence

ALIGNMENTS

RESULT 1	AZ268756	5 bp	DNA
DEFINITION	Sequence 4 from Patent WO0174342.		
ACCESSION	AZ268756.1		
VERSION	GI:16541828		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	Gichrest, B.A., Year M. and Eller, M.		
AUTHORS	Use of locally applied dna fragments		
TITLE	Patent, WO 0174342 A 11-OCT-2001;		
JOURNAL	THOMSON OF BOSTON UNIVERSITY (US)		

Pred. No. is the number of results predicted by chance to have a

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     /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 8.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AX268758/c
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ACCESSION           AX268758
VERSION             AX268758.1 GI:16541930
KEYWORDS            synthetic construct
SOURCE              artificial sequences
ORGANISM             synthetic construct
REFERENCE            Gilchrist.B.A., Vaar.M. and Eller.M.
AUTHORS             Use of locally applied dna fragments
PATENT               Patent: WO 0174342-A 7 11-OCT-2001.
JOURNAL             TRUSTEES OF BOSTON UNIVERSITY (US)
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ACCESSION           AX268755
VERSION             AX268755.1 GI:16541827
KEYWORDS            synthetic construct
SOURCE              artificial sequences
ORGANISM             synthetic construct
REFERENCE            Gilchrist.B.A., Vaar.M. and Eller.M.
AUTHORS             Use of locally applied dna fragments
PATENT               Patent: WO 0174342-A 7 11-OCT-2001.
JOURNAL             TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db
RESULT 3
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ACCESSION           AX268755/c
VERSION             AX268755.1 GI:11876656
KEYWORDS            synthetic construct
SOURCE              synthetic construct
ORGANISM             synthetic construct
REFERENCE            McIvor.R.S., Hackett.P.B. and Aguilar-Cordova,E.
AUTHORS             Vector-mediated delivery of integrating transposon sequences
PATENT               Patent: WO 0068359-A 1 11-OCT-2000.
JOURNAL             REGENTS OF THE UNIVERSITY OF MINNESOTA (US) ; BAYLOR COLLEGE OF
MEDICINE (US) ; McIvor, R. Scott (US) ; Hackett, Perry B. (US) ;
Aguilar-Cordova, Eduardo (US)
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.8e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
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DEFINITION          Sequence 7 from Patent WO0174342.
ACCESSION           AX268759
VERSION             AX268759.1 GI:16541831
KEYWORDS            synthetic construct
SOURCE              synthetic construct
ORGANISM             synthetic construct
REFERENCE            Gilchrist.B.A., Vaar.M. and Eller.M.
AUTHORS             Use of locally applied dna fragments
PATENT               Patent: WO 0174342-A 7 11-OCT-2001.
JOURNAL             TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES             Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GTATG 5
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        2 GTATG 6
Db
RESULT 5
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DEFINITION          Sequence 6 from Patent WO0068359.
ACCESSION           AX268756/c
VERSION             AX268756.1 GI:11876656
KEYWORDS            synthetic construct
SOURCE              synthetic construct
ORGANISM             synthetic construct
REFERENCE            McIvor.R.S., Hackett.P.B. and Aguilar-Cordova,E.
AUTHORS             Vector-mediated delivery of integrating transposon sequences
PATENT               Patent: WO 0068359-A 1 11-OCT-2000.
JOURNAL             REGENTS OF THE UNIVERSITY OF MINNESOTA (US) ; BAYLOR COLLEGE OF
MEDICINE (US) ; McIvor, R. Scott (US) ; Hackett, Perry B. (US) ;
Aguilar-Cordova, Eduardo (US)
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

APPLICANT: German, Thomas L.
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESS: Quarter and Brady
 ADDRESS: 10000
 CITY: Madison
 STATE: WI
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIA TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 08/08/2003, 555A
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,966
 REFERENCE/DOCKET NUMBER: 96096, 93065
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 608-251-3165
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: DNA (genomic)

Query Match 100.0% Score 5, DB 1, Length 10,
 Beat Local Similarity 100.0%, Pctd. No. 8,6e+04,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
 1 GATG 5
 6 GATG 10

RESULT 14
 US-08-250-951-1/G
 Sequence 1, Application US/08250951
 Patent No. 5332129
 GENERAL INFORMATION:
 APPLICANT: Heller, Michael J.
 NUMBER OF SEQUENCES: 10
 TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF THEIR USE
 NUMBER OF INVENTORS: 10
 ADDRESS: 12526 High Bluff Drive, Suite 300
 STREET: 12526 High Bluff Drive, Suite 300
 STATE: California
 COUNTRY: USA
 ZIP: 92130
 COMPUTER READABLE FORM:
 MEDIA TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: IBM PC compatible
 CURRENT APPLICATION DATA:
 FILING DATE: 08/08/2003, 951
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,966
 REFERENCE/DOCKET NUMBER: 96096, 93065
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 608-251-3165
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: DNA (genomic)

ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: HEL0002P
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 619-792-8477
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: DNA (genomic)
 NAME/KEY: m1ec feature
 LOCATION: 10
 OTHER INFORMATION: /note "base chromosome at the 3'
 US-08-250-951-1
 Sequence 1, Application US/08252233
 Patent No. 5332129
 GENERAL INFORMATION:
 APPLICANT: Michael J. Heller
 NUMBER OF SEQUENCES: 11
 TITLE OF INVENTION: CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
 NUMBER OF INVENTORS: 11
 ADDRESS: Lyon & Lyon
 STREET: 611 West Sixth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90017
 COMPUTER READABLE FORM:
 MEDIA TYPE: floppy disk
 OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
 SOFTWARE: Not defined (Version 1.1)
 CURRENT APPLICATION DATA:
 FILING DATE: May 4, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,966
 REFERENCE/DOCKET NUMBER: 96096, 93065
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid

Query Match 100.0% Score 5, DB 1, Length 10,
 Beat Local Similarity 100.0%, Pctd. No. 8,6e+04,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
 1 GATG 5
 8 GATG 4

```

1      Sequence 80, Application US/08646789A.
2      GENERAL INFORMATION:
3      APPLICANT: Invention, John A.
4      TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
5      CORRESPONDENCE ADDRESS:
6      ADDRESSEE: PENNIE & EMMONS
7      STREET: 1155 Avenue of the Americas
8      STATE: New York
9      COUNTRY: U.S.A.
10     CL# : 1086-2711
11     COMPTER: IBM PC COMPATIBLE
12     MEDIUM TYPE: Floppy disk
13     SOFTWARE SYSTEM: PC-DOS/MS-DOS
14     SOFTWARE APPLICATION DATA: CASE #1.0, Version #1.30
15     CURRENT APPLICATION DATA: CASE #1.0, Version #1.30
16     APPLICATION NUMBER: US/08/646,789A
17     CLASSIFICATION: May 21, 1996
18     ATTORNEY/AGENT INFORMATION:
19     NAME: Marzoch, S. Leslie
20     REFERENCE/ROCKET NUMBER: 8, 9, 973
21     TELECOMMUNICATION INFORMATION:
22     TELEPHONE: (212) 790-7090
23     TELEFAX: 6611 PENNIE
24     FAX: 6611 PENNIE
25     TYPE: nucleic acid
26     STANDARDS: single
27     MOLECULAR WEIGHT: RNA
28
29 US-08-646-789A-80
30
31 Query Match      100.0%  Score 5.  DB 3.  Length 9.
32 Query Match      44.4%  Score 17.  DB 4.  Length 17.
33
34 Matches      1 3/ 5      Conservative 2/ Mismatches 0/ Indels
35
36 DB      1 3/ 5
37
38 RESULT 11
39 US-09-048-927-1
40 Sequence 80, Application US/09048927
41 GENERAL INFORMATION:
42 APPLICANT: Glitchrise, Barbara A.
43 TITLE OF INVENTION: Use of Locally Applied DNA Fragments
44 APPLICANT: Star, Mina
45 FILE REFERENCE: H09-6832
46 CURRENT FILING DATE: US/09/048,927
47 PENDING FILING DATE: US/98-03-26
48 PENDING FILING DATE: 1998-06-03
49 PENDING FILING DATE: 1998-06-03
50 PENDING FILING DATE: 1998-06-06
51 PENDING FILING DATE: 1998-06-06
52 NUMBER OF SEQ ID NOS: 4
53
54 SEQ ID NOS:
55 1. 100%
56 2. 100%
57 3. 100%
58 4. 100%
59
60 OTHER INFORMATION: Artificial Sequence
61 OTHER INFORMATION: DNA Fragment
62
63 US-09-048-927-1

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Qy          1 QTRG 5      100.0% Score 5; Db 3, Length 9;
Db          3 QTRG 7      100.0% Seq No. 43e-07;
                                     Mismatch 0; Indels 0;
                                     Gaps 0;

RESUME 13
US-09-319-648-68/c
Sequence 68, Application US/09319648
Patent No. 6451530
GENEAL INFORMATION:
Title: Fluorescent Nucleotide Analog Halpin
Type Of Invention: Formulation for Detection of Nucleic Acid Hybridization
NUMBER OF SEQUENCES: 8
CORRESPONDENCE: US
ADDRESSER: Townsend and Tomando and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
FILE NAME: 09319648.disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION FORTH RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/09/319,648
FILING DATE: 30-Jul-1999
PRIORITY:
PRIOR APPLICATION DATA:
Application Number: US 60/032,844
FILING DATE: 13-DEC-1996
FILING IN: US 108,197
ATTORNEY/AGENT INFORMATION:
NAME: Feng, Carol
ATTORNEY NUMBER: 48,611
REFERENCE: ATTORNEY NUMBER: 61580-28100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 596-0200
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
STRANDEDNESS: atgcgta
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

Query Match Statistics: 100.0%; Score 5; DB 4; Length 9;
Matched Local 5; Conserved 0; Mismatches 0; Indels 0;
DB 7 GAPS 3

```

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1 CURRENT APPLICATION NUMBER: 02/09/142,593
2 FILING DATE: 2002-08-28; 1998
3 CLASSIFICATION: 05-0882; 1998
4 PRIOR APPLICATION: NONE
5 FILING DATE: 11-04-1997
6 PRIOR APPLICATION DATA: 00/040,664
7 FILING DATE: 11-04-1997
8 FILING DATE: 28-01-1997
9 PRIOR APPLICATION DATA: 00/065,303
10 FILING DATE: 08-08-1997
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: PCT/US98/04687
13 APPLICATION DATE: 08-08-1997
14 ATTORNEY/AGENT INFORMATION:
15 NAME: SANDBERG, VICTORIA A.
16 REFERENCE/DOCKET NUMBER: 110,00450.0101
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 412-313-0512; 126
19 INFORMATION FOR SEQ ID NO: 11:
20 SEQUENCE CHARACTERISTICS:
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TYPE: nucleic acid
24 MOLECULE TYPE: DNA (genomic)
25 05-09-142-593.11

```

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QY      1 GRNG 5
        |||||
Db      6 GRNG 2

Query Match      100.0% Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

03-08-583-276-3
Patent No. 1,587,536
GENERAL INFORMATION: US/0583276
APPLICANT: McDonald, Kevin T.
INVENTOR: McDonald, Kevin T.
APPLICANT: Tolstachev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: IMPROVED RESISTANCE GAINS AND IMPROVED
TITLE OF INVENTION: RESISTANCE GAINS AND IMPROVED
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: 19
ADDRESSED: Cecelia, Berta, Berta, Berta, Berta,
STREET: 6 Backer Farm Road
CITY: Roseland
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DATA
DATA: DATA
CLASSIFICATION: 435
FILING DATE: 05-JUN-1996
PUBLICATION DATE: 08/332,444
FILING DATE: 31-OCT-1994

```

US-08-583-276-1: GENOMIC DNA
Query Match: 100.0% Score 5; DB 2; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Sequence 8, Application US/08646789A
Patent No. 6022861
Genetic Information:
Applicant: Payman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDWARDS
STREET: 1155 Avenue of the Americas
CITY: NEW YORK
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMMENTS:
MEDICAL INFORMATION:
MEDIUM TYPE: Plumpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: In-house #1.0, Version #1.30
APPLICATION NUMBER: US/08/646_789A
FILING DATE: May 1, 1996
PRIORITY DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mitrook, S. Leslie
RESIDENCE/ADDRESS NUMBER: 8172
TELEPHONE: (212) 790-9090
TELECOMMUNICATION INFORMATION:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
TWOLOGY: linear
MUTATIONS: none
US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-80
RESULT 10

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      100.0%   Score 5; DB 3; length 9;
Query Match Similarity 100.0% Pident No. 4; SeqIdNo 7
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Qy          Db           4 GTATG 8
|||||
1 GTATG 5
|||||
1 GTATG 5
MATCHES 5
Conservative 0; Mismatches 0; Indels 0;

US-08-646-789A-8
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INVENTOR(S) ID NO.: 1
SEQUENCE CHARACTERISTICS: 1:
LENGTH: 9 bases
NUCLEIC ACID TYPE: nucleic acid
STRANDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-646-789A-8

Query Match Similarity 100.0% Pident No. 4; SeqIdNo 7
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Qy          Db           4 GTATG 8
|||||
1 GTATG 5
|||||
1 GTATG 5
MATCHES 5
Conservative 0; Mismatches 0; Indels 0;

US-08-646-789A-8
Sequence 8, Application US/08646789A
Patent No. 6022867A
GENE INFORMATION:
APPLICANT: Payman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
CORRESPONDENCE ADDRESS: 101
ADDRESSER: PENNIE & EDWARDS
STREET: 1155 Avenue of the Americas
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMMENTS: SEQUENCE FROM:
MEDIUM TYPE: plodpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: In-house #1.0, Version #1.30
APPLICATION NUMBER: US/08/646_789A
FILING DATE: May 11, 1996
PRIORITY DATE: 05/11/96
ATTORNEY/AGENT INFORMATION:
NAME: Mitrook, S. Leslie
REFERENCE ORIGIN NUMBER: 6523-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66141 BSB4
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-789A-8

Query Match Similarity 100.0% Pident No. 4; SeqIdNo 7
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Qy          Db           4 GTATG 5
|||||
1 GTATG 5
MATCHES 5
Conservative 0; Mismatches 0; Indels 0;

US-08-646-789A-80
RESULT 10

```

[illegible]

```

US-08-583-276-1: GENOMIC DNA
Query Match: 100.0% Score 5; DB 2; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Sequence 8, Application US/08646789A
Patent No. 6022861
Genetic Information:
Applicant: Payman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDWARDS
STREET: 1135 Avenue of the Americas
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMMENTS:
MEDICAL INFORMATION:
COMBINATION:
OPERATING SYSTEM: IBM PC compatible
CURRENT APPLICATION DATA: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/646_789A
FILING DATE: May 1, 1996
PRIORITY DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
RESIDENCE/ADDRESS NUMBER: 8, 372
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66141 BSB4
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOWARDX: linear
MODIFICATIONS: DNA
US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-80
RESULT 10

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[illegible]

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US-08-583-276-1: GENOMIC DNA
Query Match: 100.0% Score 5; DB 2; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Sequence 8, Application US/08646789A
Patent No. 6022861
Genetic Information:
Applicant: Payman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDWARDS
STREET: 1155 Avenue of the Americas
CITY: NEW YORK
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMMENTS:
MEDICAL INFORMATION:
MEDIUM TYPE: Plumpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: In-house #1.0, Version #1.30
APPLICATION NUMBER: US/08/646_789A
FILING DATE: May 1, 1996
PRIORITY DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mitrook, S. Leslie
RESIDENCE/ADDRESS NUMBER: 8172
TELEPHONE: (212) 790-9090
TELECOMMUNICATION INFORMATION:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOWARDX: linear
MODIFICATIONS: DNA
US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Id. Similarity: 100.0% Pos. Percent: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-80
RESULT 10

```

```

US-08-583-276-1: GENOMIC DNA
Query Match: 100.0% Score 5; DB 2; length 9;
Seq. Ident. Similarity: 100.0% Pct. Ident: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Ident. Similarity: 100.0% Pct. Ident: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-8
Sequence 8, Application US/08646789A
Patent No. 6022861
Genetic Information:
Applicant: Payman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDWARDS
STREET: 1155 Avenue of the Americas
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMMENTS:
MEDICAL INFORMATION:
MEDIUM TYPE: Plumpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: In-house #1.0, Version #1.30
APPLICATION NUMBER: US/08/646_789A
FILING DATE: May 1, 1996
PRIORITY DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mitrook, S. Leslie
RESIDENCE/ADDRESS NUMBER: 6372
TELEPHONE: (212) 790-9090
TELECOMMUNICATION INFORMATION:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOWARDX: linear
MOTIF:
OTHER: DNA
US-08-646-789A-8
Query Match: 100.0% Score 5; DB 3; length 9;
Seq. Ident. Similarity: 100.0% Pct. Ident: 100.0%
Matches 5; Conservative 0; Mismatches 0; Indels 0;
QY      1 GTATG 5
DB      4 GTATG 8

US-08-646-789A-80
RESULT 10

```


QY 1 GIVING 5
DB 1 GIVING 5

RESULT 2

US-09-048-927-4
Sequence 10, Application US/09048927
GENERAL INFORMATION:
APPLICANT: GlaxoSmithKline, Barbara A.
APPLICANT: GlaxoSmithKline, Barbara A.
APPLICANT: GlaxoSmithKline, Barbara A.
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: 8094-6442, US/09/048,927
CURRENT FILING DATE: 1998-03-26
EXAMINER FILING DATE: 1998-06-03, 697,697
EXAMINER FILING DATE: 1998-06-03, 697,697
EXAMINER FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 4
SEQ ID NO. 4: PARASITO for Windows version 3.0
LENGTH: 5
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: DNA Fragment
US-09-048-927-4

Query Match
Best Local Similarity 100.0%; Seq. ID No. 8,26+07; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIVING 5
DB 1 GIVING 5

RESULT 3

US-09-048-927-4
Sequence 20, Application US/09048927
Patent No. 6440671
GENERAL INFORMATION:
APPLICANT: GlaxoSmithKline, Barbara A.
APPLICANT: GlaxoSmithKline, Barbara A.
APPLICANT: GlaxoSmithKline, Barbara A.
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: 8094-6442, US/09/048,927
CURRENT FILING DATE: 1998-03-26
EXAMINER FILING DATE: 1998-06-03, 697,697
EXAMINER FILING DATE: 1998-06-03, 697,697
EXAMINER FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 4
SEQ ID NO. 4: PARASITO for Windows version 3.0
LENGTH: 5
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: DNA Fragment
US-09-048-927-4

RESULT 4

US-08-615-170-10/C
Sequence 10, Application US/08615170
Patent No. 5716776
GENERAL INFORMATION:
APPLICANT: GlaxoSmithKline, Barbara A.
APPLICANT: GlaxoSmithKline, Barbara A.
APPLICANT: GlaxoSmithKline, Barbara A.
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: 8094-6442, US/09/048,927
CURRENT FILING DATE: 1998-03-26
EXAMINER FILING DATE: 1998-06-03, 697,697
EXAMINER FILING DATE: 1998-06-03, 697,697
EXAMINER FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 4
SEQ ID NO. 4: PARASITO for Windows version 3.0
LENGTH: 5
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: DNA Fragment
US-09-048-927-4


```

1 APPLICANT: Ribozyme Pharmaceuticals Inc.
2 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
3 TO HIV INFECTION AND HEPATITIS C VIRUS INFECTION
4 CURRENT APPLICATION NUMBER: US/09/817,879
5 CURRENT FILING DATE: 2001-03-26
6 NUMBER OF SEQ ID NOS: 9703
7 SOURCE: Ribozyme version 3.0
8 SEQ ID NO: 4624
9 LENGTH: 13
10 ORGANISM: Artificial Sequence
11 FEATURE:
12 NAME/KEY: misc_feature
13 OTHER INFORMATION: oligonucleotide substrate
14
15 Query Match
16 Best Local Similarity 100.0% Score 7 DB 13 Length 13
17 Matched 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
18
19 DB 6 ACNUCA 12
20
21 RESULT 15
22 US-09-875-440-22/c
23 Sequence 22 US Application US/09875440
24 Sequence 22 US Patent US/020165241
25 GENERAL INFORMATION:
26 APPLICANT: Reinhard, Christoph
27 APPLICANT: Reinhard, Christoph
28 APPLICANT: Reinhard, Christoph
29 APPLICANT: Reinhard, Christoph
30 APPLICANT: Reinhard, Christoph
31 APPLICANT: Reinhard, Christoph
32 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
33 HIV INFECTION
34 CURRENT APPLICATION NUMBER: US/09/875,440
35 FILE REFERENCE: PP-01701, 002/20010, 522
36 NUMBER FILING DATE: 2001-06-05
37 NUMBER OF SEQ ID NOS: 22
38 SOFTWARE: PatsEQ for Windows Version 4.0
39 SEQ ID NO: 22
40 LENGTH: 14
41 ORGANISM: Artificial Sequence
42 FEATURE:
43 OTHER INFORMATION: Oligonucleotide NET-4 oligo 868 used for in-vitro
44 hybridization
45 US-09-875-440-22

```

```

26 Query Match
27 Best Local Similarity 100.0% Score 7 DB 10 Length 14
28 Matched 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
29
30 DB 13 ACNUCA 7
31
32 Query
33 1 ACNUCA 7
34 |||||
35 |||||
36 |||||
37 |||||
38 |||||
39 |||||
40 |||||
41 |||||
42 |||||
43 |||||
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Job time : 82.6076 secs

OY 1 AACTATCA 7
DB 10 AACTATCA 4

US-10-033-143-1431/C
Publication No. US2003015151A1

GENERAL INFORMATION:

APPLICANT: GENZYME CORPORATION

APPLICANT: GENZYME CORPORATION

APPLICANT: SHANKARA SRINIVAS

TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

FILE REFERENCE: CA0201038; US/6/003,145

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR FILING DATE: 1999-05-18

INVENTOR: SRI, SUDHAKAR

INVENTOR: SRI, SUDHAKAR

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1423

ORGANISM: Homo sapiens

TYPE: DNA

US-10-033-143-143

Query Match 100.0%; Score 7; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTATCA 7
DB 7 AACTATCA 1

US-10-033-143-143

Publication No. US20030129241A1

GENERAL INFORMATION:

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

TITLE OF INVENTION: IMMUNIZING USES OF LAM-MODIFIED OLIGONUCLEOTIDES IN

FILE REFERENCE: 55704 (45120)

CURRENT APPLICATION NUMBER: US/6/0150,779A

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 60/293,830

INVENTOR: KOCHE, HERBRICK

INVENTOR: KOCHE, HERBRICK

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 12

ORGANISM: Artificial Sequence

FEATURE INFORMATION: Description of Artificial Sequence Synthetic

OTHER INFORMATION: oligonucleotide

US-10-033-143-143

Query Match 100.0%; Score 7; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTATCA 7
DB 11 AACTATCA 5

US-09-540-843-3
Publication No. US20030129241A1

GENERAL INFORMATION:

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

TITLE OF INVENTION: IMMUNIZING USES OF LAM-MODIFIED OLIGONUCLEOTIDES IN

FILE REFERENCE: 55704 (45120)

CURRENT APPLICATION NUMBER: US/6/0150,779A

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 60/293,830

PRIOR FILING DATE: 2001-05-18

INVENTOR: KOCHE, HERBRICK

INVENTOR: KOCHE, HERBRICK

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 12

ORGANISM: Artificial Sequence

FEATURE INFORMATION: Description of Artificial Sequence Synthetic

OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone

US-10-033-143-143

Query Match 100.0%; Score 7; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTATCA 7
DB 11 AACTATCA 5

US-09-540-843-3

Publication No. US20030129241A1

GENERAL INFORMATION:

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

TITLE OF INVENTION: IMMUNIZING USES OF LAM-MODIFIED OLIGONUCLEOTIDES IN

FILE REFERENCE: 55704 (45120)

CURRENT APPLICATION NUMBER: US/6/0150,779A

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 60/293,830

INVENTOR: KOCHE, HERBRICK

INVENTOR: KOCHE, HERBRICK

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4824

LENGTH: 12

ORGANISM: Artificial Sequence

FEATURE INFORMATION: Description of Artificial Sequence Synthetic

OTHER INFORMATION: oligonucleotide substrate

US-09-540-843-3

Query Match 100.0%; Score 7; DB 11; Length 13;

Best Local Similarity 77.4%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTATCA 7
DB 6 AACTATCA 12

US-09-540-843-3

Publication No. US20030129241A1

GENERAL INFORMATION:

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

APPLICANT: KOCHE, HERBRICK

TITLE OF INVENTION: IMMUNIZING USES OF LAM-MODIFIED OLIGONUCLEOTIDES IN

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Db          1 MATCHA 7
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RESULT 3
US-10-122-633-7
Sequence 7, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Glitcher, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Year, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
FILE REFERENCE: 0054,1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
PRIOR FILING DATE: 1995-06-06/09/540,843
PRIOR APPLICATION NUMBER: PCT/US01/0162
PRIOR FILING DATE: 2001-03-30
SOFTWARE: ParasO for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPER: DNA
FEATURE: Artificial Sequence
ORGANISM: Homo sapiens
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-636-7
Query Match          100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pctd No. 48+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MATCHA 7
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Query Match          100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pctd No. 48+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MATCHA 7
-----
RESULT 4
US-10-122-633-7
Sequence 7, Application US/10122633
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Glitcher, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Year, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
FILE REFERENCE: 0054,1088-018
CURRENT APPLICATION NUMBER: US/10/122,633
PRIOR FILING DATE: 2002-04-12/09/540,843
PRIOR APPLICATION NUMBER: PCT/US01/0162
PRIOR FILING DATE: 2001-03-30
SOFTWARE: ParasO for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
TYPER: DNA
FEATURE: Artificial Sequence
ORGANISM: Homo sapiens
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7
Query Match          100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pctd No. 48+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MATCHA 7
-----
RESULT 5
US-10-122-630-1
Sequence 1, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Glitcher, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Year, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
FILE REFERENCE: 0054,1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
PRIOR FILING DATE: 1995-06-06/09/540,843
PRIOR APPLICATION NUMBER: PCT/US96/00386
PRIOR FILING DATE: 1998-03-26/09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
SOFTWARE: ParasO for Windows Version 4.0
SEQ ID NO 1
LENGTH: 9
TYPER: DNA
FEATURE: Artificial Sequence
ORGANISM: Homo sapiens
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7
Query Match          100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pctd No. 48+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MATCHA 7
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GenCode version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 / Search time 81.6076 Seconds

286.956 Million call updates/sec

Title: US-09-540-843-3

Perfect score: 7

Sequence: 1 gaccgga 7

Scoring table: IDENTITY NUC

Gapop 10.0 / Repeat 1.0

Searched: 2863441 seqs, 171067930 reads/as

Total number of hits according chosen parameters: 998502

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Letting filter: 45 summaries

Database: Published Application MA.

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- 2: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 3: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 4: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 5: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 6: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 7: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 8: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 9: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 10: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 11: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 12: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 13: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 14: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 15: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 16: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 17: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*
- 18: /cgn2_6/prodata/1/pubmap/US06_NFW_PUB seq.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7 100.0	7 15	US-10-122-630-3	Sequence 3, Appl1
2	7 100.0	7 15	US-10-122-630-7	Sequence 3, Appl1
3	7 100.0	7 15	US-10-122-630-5	Sequence 3, Appl1
4	7 100.0	7 15	US-10-122-630-3	Sequence 3, Appl1
5	7 100.0	9 15	US-10-122-630-1	Sequence 3, Appl1
6	7 100.0	9 15	US-10-122-630-1	Sequence 3, Appl1
7	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
8	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
9	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
10	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
11	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
12	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
13	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
14	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1
15	7 100.0	10 13	US-10-122-630-1	Sequence 3, Appl1

16	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
17	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
18	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
19	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
20	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
21	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
22	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
23	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
24	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
25	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
26	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
27	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
28	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
29	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
30	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
31	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
32	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
33	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
34	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
35	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
36	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
37	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
38	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
39	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
40	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
41	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
42	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
43	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
44	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App
45	7 100.0	15 9	US-09-504-231A-528	Sequence 527, App

ALIGNMENTS

US-10-122-630-3
Sequence 3, Application US/10122630
GENERAL INFORMATION:
APPLICANT: GlaxoSmithKline
APPLICANT: GlaxoSmithKline
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
REFERENCE: US 1,088,016/0122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/0162
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTED for Windows Version 4.0
SEQ ID NO: 3
TYPE: DNA
ORGANISM: Artificial Sequence
COMMENT: Synthetic DNA Fragment
US-10-122-630-3
Query Match: 100.0% Score 7, DB 15 Length 7,
Similarity: 100.0% Score 7, DB 15 Length 7,
Mismatch: 0, Mismatches 0, Gaps 0,
Matches 7, Conservative 0, Indels 0,
Gaps 0,
1 MATCH 7

LOCATION: (1)...(12)
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Flexible hinge
 Patent No. 6095405
 US-09-290-449-15

Query Match 88.3% Score 8; DB 3; Length 12;
 Best Local Similarity 100.0%; Pctd No. 1,26/40
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 3 AGCGAGT 10

RESULT 14
 US-08-182-968A-169/C
 Sequence No. 169 Application US/08182968A
 Patent No. 6095405
 GENERAL INFORMATION:
 APPLICANT: Dreyer, Kenneth G.
 TITLE OF INVENTION: INHIBITING HEPATITIS C
 TITLE OF INVENTION: VIRUS REPLICATION
 NUMBER OF SEQUENCES: 497
 CORRESPONDING ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: San Diego
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIAN TYPE: storage
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 FILING DATE: 13-JANUARY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/882,888
 ATTORNEY/AGENT INFORMATION:
 NAME: Wadburg, Richard J.
 REGISTRATION NUMBER: 33,352
 TELEPHONE: (213) 489-1600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: 67-3510 955-0440
 INFORMATION FOR SEQ ID NO: 168:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-182-968A-169

Query Match 88.3% Score 8; DB 1; Length 15;
 Best Local Similarity 100.0%; Pctd No. 1,36/40;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 13 AGCGAGT 6

RESULT 15
 US-08-182-968A-169/C

Sequence 169 Application US/08182968A
 Patent No. 6095405
 GENERAL INFORMATION:
 APPLICANT: Dreyer, Kenneth G.
 TITLE OF INVENTION: INHIBITING HEPATITIS C
 TITLE OF INVENTION: VIRUS REPLICATION
 NUMBER OF SEQUENCES: 497
 CORRESPONDING ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: San Diego
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIAN TYPE: storage
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 FILING DATE: 13-JANUARY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/882,888
 ATTORNEY/AGENT INFORMATION:
 NAME: Wadburg, Richard J.
 REGISTRATION NUMBER: 33,352
 TELEPHONE: (213) 489-1600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: 67-3510 955-0440
 INFORMATION FOR SEQ ID NO: 169:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-182-968A-169

Query Match 88.3% Score 8; DB 1; Length 15;
 Best Local Similarity 100.0%; Pctd No. 1,36/40;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 10 AGCGAGT 3

Search completed: January 1, 2004, 00:32:18
 Job time : 35.0858 secs


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? FILING DATE: APR11 16, 1998
? PRIORITY DATE: APR11 16, 1998
? PRIORITY APPLICATION NO.: NONE
? APPLICATION NUMBER:
?
? FILING DATE:
? ATORNEY/AGENT INFORMATION:
? NAME: A. TAYLOR, JR.
? REGISTRATION NUMBER: 39,195
? TELEPHONE: (919) 493-8000
? TELEFAX: (919) 493-8000
?
? INFORMATION FOR SEQ ID NO: 33:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 28 base pairs
? STRANDEDNESS: single
? TOPOLOGY: linear
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? US-09-061-7684-13
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? Beat Local Similarity: 100.0%; Score 9; DB 3; Length 28;
? Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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? 1 TTAGCGAGT 9
? 7 TTAGCGAGT 15

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? RESULT 11
? Sequence 20, Application US/0810156
? Patent No. 5648243
?
? GENERAL INFORMATION:
? APPLICANT: Nathan, Margaret
? APPLICANT: Shari, Moshe
? NUMBER OF INVENTORS: 2
? NUMBER OF RESOURCES: 1
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Rhone-Poulenc Rorer Legal Department
? CITY: Collegeville
? STATE: PA
? COUNTRY: USA
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER SYSTEM: Microsoft Windows 7.0
? SOFTWARE: Microsoft Word Version 5.0 (PatentIn)
?
? CURRENT APPLICATION DATA:
? PUBLICATION NUMBER: US/08/10,356
? CLASSIFICATION: 800
?
? PRIORITY APPLICATION DATA: US/07/737,853
? FILING DATE: 31-JUL-1993
? ATORNEY/AGENT INFORMATION:
? NAME: Goodman, Roseanne
? REGISTRATION NUMBER: 4285
? TELEPHONE: (919) 493-8000
? TELEFAX: (919) 493-8000
? INFORMATION FOR SEQ ID NO: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 100 bp
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? US-08-310-356-20

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Best Local Similarity 100.0%; Pref. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 TAGCGAAT 9
DB 9 TAGCGAAT 17

RESULT 6
US-09-416-0504-15/c
Sequence 15; Application US/094160504
GENERAL INFORMATION:
APPLICANT: KIM, Soo Young
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factors
CURRENT FILING DATE: 1999-10-12
PRIORITY FILING DATE: 1999-10-12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 24
ORGANISM: Arabidopsis thaliana

US-09-416-0504-15
Query Match
Best Local Similarity 100.0%; Pref. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 TAGCGAAT 9
DB 17 TAGCGAAT 9

RESULT 7
US-09-664-800-15/c
Sequence 15; Application US/09664800
GENERAL INFORMATION:
APPLICANT: KIM, Soo Young
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factor
CURRENT FILING DATE: 1999-10-12
PRIORITY FILING DATE: 1999-10-12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 24
ORGANISM: Arabidopsis thaliana

US-09-664-800-15
Query Match
Best Local Similarity 100.0%; Pref. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 TAGCGAAT 9
DB 17 TAGCGAAT 9

RESULT 8
US-09-665-309-15/c
Sequence 15; Application US/09665309
GENERAL INFORMATION:
APPLICANT: KIM, Soo Young
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factor
CURRENT FILING DATE: 1999-10-12
PRIORITY FILING DATE: 1999-10-12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 24
ORGANISM: Arabidopsis thaliana

US-09-665-309-15
Query Match
Best Local Similarity 100.0%; Pref. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 TAGCGAAT 9
DB 17 TAGCGAAT 9

CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/416,050
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 24
ORGANISM: Arabidopsis thaliana

US-09-665-309-15
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Best Local Similarity 100.0%; Pref. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 TAGCGAAT 9
DB 17 TAGCGAAT 9

RESULT 9
US-09-661-569-15/c
Sequence 15; Application US/09661569
GENERAL INFORMATION:
APPLICANT: KIM, Soo Young
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factor
CURRENT FILING DATE: 2000-09-19
PRIORITY FILING DATE: 1999-10-12
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 24
ORGANISM: Arabidopsis thaliana

US-09-661-569-15
Query Match
Best Local Similarity 100.0%; Pref. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 TAGCGAAT 9
DB 17 TAGCGAAT 9

RESULT 10
US-09-661-768A-33
Sequence 33; Application US/09661768A
GENERAL INFORMATION:
APPLICANT: BASH, ALAN R.
APPLICANT: JISKA, WILLIAM E.
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSES: ALEX A. TAYLOR, JR.
CROSS STREET 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707

US-09-661-768A-33
Query Match
Best Local Similarity 100.0%; Pref. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 TAGCGAAT 9
DB 17 TAGCGAAT 9

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
OPERATING SYSTEM: Windows 95/NT
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,768A

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-232-3276-20

Query Match 100.0%; Score 11; DB 13;
Local Similarity 100.0%; Positives 4; Negatives 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OTTACGETTING 11
DB 13 OTTACGETTING 3

Search completed: January 1, 2004, 01:10:37
Job time: 129.241 secs

REGISTRATION NUMBER: 32,844
 REFERENCE/ROCKET NUMBER: 015389-000821US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 FAX: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: DNA
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-037-3212
 MOLECULE TYPE: RNA

Query Match 100.0% Score 11; DB 9; Length 11;
 Best Local Similarity 100.0% Pct. No. 4.7e+03
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAGGCTTG 11
 Db 11 GTCAGGCTTG 11

RESULT 2
 US-10-255-535-4
 Sequence 63, Application US/0993370
 Publication No. US2000013814A1
 INVENTION: OLIGONUCLEOTIDE CONJUGATES
 APPLICANT: URMANN, GERHARD
 APPLICANT: BREITPH, GERHARD
 TITLE OF INVENTION: POLYMER NUCLEIC ACID DERIVATIVES AND AGENTS AND
 TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
 FILE REFERENCE: 02481.1742 SEQUENCE LISTING
 CURRENT FILING DATE: 2001-04-17
 NUMBER OF SEQ ID NOS: 64
 PRIOR FILING DATE: 2001-04-17
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 11
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: nucleotide
 OTHER INFORMATION: base sequence of PNA derivatives that bind to
 OTHER INFORMATION: viral and cellular targets
 US-09-035-37063

Query Match 100.0% Score 11; DB 11; Length 11;
 Best Local Similarity 100.0% Pct. No. 4.7e+03
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAGGCTTG 11
 Db 11 GTCAGGCTTG 11

RESULT 3
 US-10-255-535-4
 Sequence 4, Application US/1025535
 Publication No. US2000013814A1
 INVENTION: OLIGONUCLEOTIDE CONJUGATES
 APPLICANT: GECON CORPORATION
 APPLICANT: GRAYZOV, SERGEI
 APPLICANT: TOLMAN, RICHARD L.
 APPLICANT: MORIN, GREGG B.
 TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
 CURRENT FILING DATE: 2002-09-25
 CURRENT APPLICATION NUMBER: US/010255,535
 PRIOR APPLICATION NUMBER: PCT/US02/09138
 PRIOR FILING DATE: 2002-03-21

PRIOR APPLICATION NUMBER: US 60/278,122
 PRIOR FILING DATE: 2001-03-23
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.1
 LENGTH: 11
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: oligonucleotide
 US-10-255-535-4

Query Match 100.0% Score 11; DB 11; Length 11;
 Best Local Similarity 100.0% Pct. No. 4.7e+03
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAGGCTTG 11
 Db 11 GTCAGGCTTG 11

RESULT 4
 US-10-255-535-14
 Sequence 1, Application US/1055555
 Publication No. US2000013814A1
 INVENTION: OLIGONUCLEOTIDE CONJUGATES
 APPLICANT: Gecon Corporation
 APPLICANT: Pongracz, Kristina
 APPLICANT: Tolman, Richard L.
 TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
 FILE REFERENCE: 072/002P
 CURRENT APPLICATION NUMBER: US/10/255,535
 PRIOR APPLICATION NUMBER: PCT/US02/09138
 PRIOR FILING DATE: 2002-03-21
 PRIOR FILING DATE: 2002-03-21/0270,122
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.1
 LENGTH: 11
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: oligonucleotide
 US-10-255-535-14

Query Match 100.0% Score 11; DB 11; Length 11;
 Best Local Similarity 100.0% Pct. No. 4.7e+03
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAGGCTTG 11
 Db 11 GTCAGGCTTG 11

RESULT 5
 US-10-358-935-2/C
 Sequence 1, Application US/0159935
 Publication No. US20000135076A1
 INVENTION: OLIGONUCLEOTIDE CONJUGATES
 APPLICANT: VILLEGORTEU, BRYANT
 APPLICANT: FUND, NALIER
 APPLICANT: ANDREWS, WILLIAM H.
 TITLE OF INVENTION: Nucleic Acid Telomerase
 CURRENT FILING DATE: 2002-03-21
 CURRENT APPLICATION NUMBER: PCT/US02/09138
 ADDRESSER: Townsend and Crew LLP
 STREET: Two Embarcadero Center, 15th Floor
 CITY: San Francisco

